STIC Search Report
Biotech-Chem Library

TO: Quang Nguyen
Location: rem/2E81/2C70
Art Unit: 1633
Thursday, November 02, 2006
Case Serial Number: 10/706798

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Nguyen,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
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Run on: November 1, 2006, 19:39:18 ; Search time 1837.86 Seconds
(without alignments)
2887.948 Million cell updates/sec

Title: US-10-706-798-1
Perfect score: 83
Sequence: 1 ccuggaguaaaguaguagcagc..........gcugccucaaaauacaagg 83

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 3197371019525 residues

Total number of hits satisfying chosen parameters: 12732272

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :   GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	83	2	CS185098	CS185098 Sequence
2	83	100.0	83	2	CS188802	CS188802 Sequence
3	83	100.0	63	2	AY866304	AY866304 Lemur cat
4	83	100.0	712	5	AY866308	AY866308 Lagothrix
5	83	100.0	747	5	AY866306	AY866306 Pongo pyg
6	83	100.0	825	5	AY866302	AY866302 Saguinus
7	83	100.0	836	5	AY866299	AY866299 Ateles ge
8	83	100.0	871	5	AY866301	AY866301 Macaca ne
9	83	100.0	896	5	AY866305	AY866305 Macaca mu
10	83	100.0	901	5	AY866300	AY866300 Gorilla g
11	83	100.0	902	5	AY866307	AY866307 Pan trogl
12	83	100.0	914	5	AY866303	AY866303 Pan panis
13	83	100.0	153092	5	AC069475	AC069475 Homo sapi
14	83	100.0	154868	5	AF334404	AF334404 Homo sapi
15	83	100.0	154887	5	AL137060	AL137060 Human DNA
16	83	100.0	184155	12	AC155017	AC155017 Bos tauru
17	83	100.0	235659	12	AC152429	AC152429 Bos tauru
18	83	100.0	347503	5	AF279660	AF279660 Homo sapi
19	83	100.0	350000	5	AF440619	AF440619 Homo sapi
20	79	95.2	108	2	CS188801	CS188801 Sequence
21	71.8	86.5	172152	6	AC154660	AC154660 Mus muscu
22	40	48.2	40	2	CS189094	CS189094 Sequence
23	40	48.2	40	2	CS189095	CS189095 Sequence
24	35.8	43.1	150820	11	AC154053	AC154053 Ictalurus
25	35.2	42.4	97210	11	AL606727	AL606727 Zebrafish
26	35.2	42.4	214290	11	BX294379	BX294379 Zebrafish
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32	33.4	40.2	825	5	AY866302	AY866302 Saguinus
33	33.4	40.2	836	5	AY866299	AY866299 Ateles ge
34	33.4	40.2	871	5	AY866301	AY866301 Macaca ne
35	33.4	40.2	896	5	AY866305	AY866305 Macaca mu
36	33.4	40.2	901	5	AY866300	AY866300 Gorilla g
37	33.4	40.2	902	5	AY866307	AY866307 Pan trogl
38	33.4	40.2	914	5	AY866303	AY866303 Pan panis
39	33.4	40.2	153092	5	AC069475	AC069475 Homo sapi
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42	33.4	40.2	188644	11	CR478286	CR478286 Zebrafish
43	33.4	40.2	184155	12	AC155017	AC155017 Bos tauru
44	33.4	40.2	235659	12	AC152429	AC152429 Bos tauru
45	33.4	40.2	347503	5	AF279660	AF279660 Homo sapi

ALIGNMENTS

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RESULT 1
LOCUS       CS185098                83 bp    RNA     linear   PAT 01-NOV-2005
DEFINITION  CS185098 Sequence 72 from Patent WO2005098029.
ACCESSION   CS185098
VERSION     CS185098.1  GI:78585070
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jacobsen,N.
  TITLE     NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL INTERFERING
            RNAS
  JOURNAL   Patent: WO 2005098029-A 72 20-OCT-2005;
            Exigon A/S (DK)
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Qy         61 UGUGCCUGCCUCAAAAAAUACAAGG 83
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Db         61 TGTGCTGCCTCAAAAAATACAAGG 83

RESULT 2
LOCUS       CS188802                83 bp    DNA     linear   PAT 04-NOV-2005
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DEFINITION   Sequence 33 from Patent WO2005078139.
ACCESSION   CS188802
VERSION   CS188802.1   GI:80749791
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE   1
  AUTHORS   Croce,C.M.
  JOURNAL   Patent: WO 2005078139-A 33 25-AUG-2005;
              THOMAS JEFFERSON UNIVERSITY (US)
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Qy   61 UGUGCUGCUCCUCAAAAAAAUACAAGG 83
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Db   61 TGTGCTGCCTCAAAAAAATACAAGG 83

RESULT 3
LOCUS   AY866304   663 bp   DNA   linear   PRI 24-JAN-2005
DEFINITION   Lemur catta microRNA mir-15a and microRNA mir-16-1 genes, complete
              sequence.
ACCESSION   AY866304
VERSION   AY866304.1   GI:57903106
KEYWORDS   .
SOURCE   Lemur catta (ring-tailed lemur)
  ORGANISM   Lemur catta
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini;
              Lemuriformes; Lemuridae; Lemur.
REFERENCE   1 (bases 1 to 663)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
              Plasterk,R.H. and Cuppen,E.
  TITLE   Phylogenetic Shadowing and Computational Identification of Human
              microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
   PUBMED   15652478
REFERENCE   2 (bases 1 to 663)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
              Plasterk,R.H. and Cuppen,E.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
              3584 CT, The Netherlands
FEATURES   Location/Qualifiers
     source   1..663
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                     /mol_type="genomic DNA"
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     misc_RNA   463..484
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     misc_RNA   590..663
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                     /note="based on Homo sapiens mir-16-1"
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Db   510 TGTGCTGCCTCAAAAAAATACAAGG 532

RESULT 4
LOCUS   AY866308   712 bp   DNA   linear   PRI 24-JAN-2005
DEFINITION   Lagothrix lagotricha microRNA mir-15a and microRNA mir-16-1 genes,
              complete sequence.
ACCESSION   AY866308
VERSION   AY866308.1   GI:57903110
KEYWORDS   .
SOURCE   Lagothrix lagotricha (common woolly monkey)
  ORGANISM   Lagothrix lagotricha
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
              Cebidae; Atelinae; Lagothrix.
REFERENCE   1 (bases 1 to 712)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
              Plasterk,R.H. and Cuppen,E.
  TITLE   Phylogenetic Shadowing and Computational Identification of Human
              microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
   PUBMED   15652478
REFERENCE   2 (bases 1 to 712)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
              Plasterk,R.H. and Cuppen,E.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
              3584 CT, The Netherlands
FEATURES   Location/Qualifiers
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Qy   61 UGUGCUGCUCCUCAAAAAAAUACAAGG 83
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Db   450 TGTGCTGCCTCAAAAAAATACAAGG 472

RESULT 5

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LOCUS       AY866306                 747 bp    DNA     linear   PRI 24-JAN-2005
DEFINITION  Pongo pygmaeus microRNA mir-15a and microRNA mir-16-1 genes,
            complete sequence.
ACCESSION   AY866306
VERSION     AY866306.1  GI:57903108
KEYWORDS    .
SOURCE      Pongo pygmaeus (orangutan)
  ORGANISM  Pongo pygmaeus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pongo.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
  TITLE     Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
   PUBMED   15652478
REFERENCE   2  (bases 1 to 747)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H.A. and Cuppen,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
            3584 CT, The Netherlands
FEATURES             Location/Qualifiers
     source          1..747
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     misc_RNA        490..511
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     misc_RNA        617..705
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Qy   61 UGUGCUGCCUCAAAAAUACAAGG 83
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Db  537 TGTGCTGCCTCAAAAATACAAGG 559


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LOCUS       AY866302                 825 bp    DNA     linear   PRI 24-JAN-2005
DEFINITION  Saguinus labiatus microRNA mir-15a and microRNA mir-16-1 genes,
            complete sequence.
ACCESSION   AY866302
VERSION     AY866302.1  GI:57903104
KEYWORDS    .
SOURCE      Saguinus labiatus (red-chested mustached tamarin)
  ORGANISM  Saguinus labiatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
            Callitrichidae; Saguinus.
REFERENCE   1  (bases 1 to 825)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
  TITLE     Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
   PUBMED   15652478
REFERENCE   2  (bases 1 to 825)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H.A. and Cuppen,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
            3584 CT, The Netherlands
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Db  448 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGGATTTTGAAAAAGGTGCAGGCCATAT 507

Qy   61 UGUGCUGCCUCAAAAAUACAAGG 83
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Db  508 TGTGCTGCCTCAAAAATACAAGG 530


RESULT 7
LOCUS       AY866299                 836 bp    DNA     linear   PRI 24-JAN-2005
DEFINITION  Ateles geoffroyi microRNA mir-15a and microRNA mir-16-1 genes,
            complete sequence.
ACCESSION   AY866299
VERSION     AY866299.1  GI:57903101
KEYWORDS    .
SOURCE      Ateles geoffroyi (black-handed spider monkey)
  ORGANISM  Ateles geoffroyi
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
            Cebidae; Atelinae; Ateles.
REFERENCE   1  (bases 1 to 836)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
  TITLE     Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
   PUBMED   15652478
REFERENCE   2  (bases 1 to 836)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H.A. and Cuppen,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
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RESULT 8
AY866301

LOCUS       AY866301               871 bp    DNA     linear   PRI 24-JAN-2005
DEFINITION  Macaca nemestrina microRNA mir-15a and microRNA mir-16-1 genes,
            complete sequence.
ACCESSION   AY866301
VERSION     AY866301.1  GI:57903103
KEYWORDS    .
SOURCE      Macaca nemestrina (pig-tailed macaque)
ORGANISM    Macaca nemestrina
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
  TITLE     Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
  PUBMED    15652478
REFERENCE   2  (bases 1 to 871)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
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ORIGIN

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Qy     61    UGUGCUGCCUCAAAAAUACAAGG 83
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Db    533    TGTGCTGCCTCAAAAATACAAGG 555
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RESULT 9
AY866305

LOCUS       AY866305               896 bp    DNA     linear   PRI 24-JAN-2005
DEFINITION  Macaca mulatta microRNA mir-15a and microRNA mir-16-1 genes,
            complete sequence.
ACCESSION   AY866305
VERSION     AY866305.1  GI:57903107
KEYWORDS    .
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM    Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
  TITLE     Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
  PUBMED    15652478
REFERENCE   2  (bases 1 to 896)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
            3584 CT, The Netherlands
FEATURES             Location/Qualifiers
     source          1..896
                     /organism="Macaca mulatta"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9544"
     misc_RNA        462..544
                     /product="precursor microRNA mir-15a"
                     /note="based on Homo sapiens mir-15a"
     misc_RNA        475..496
                     /product="microRNA mir-15a"
     misc_RNA        602..690
                     /product="precursor microRNA mir-16-1"
                     /note="based on Homo sapiens mir-16-1"
     misc_RNA        615..636
                     /product="microRNA mir-16-1"

ORIGIN

Query Match     100.0%;  Score 83;  DB 5;  Length 896;
Best Local Similarity   73.5%;  Pred. No. 1.6e-20;  Indels 0;  Gaps 0;
Matches 61;  Conservative 22;  Mismatches 0;

Qy      1    CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
             ||||||||||||||||||||||||||||||||||::||||||||||||||||||||||||:|:
Db    462    CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGTGGATTTTGAAAAGGTGCAGGCCATAT 521

Qy     61    UGUGCUGCCUCAAAAAUACAAGG 83
             :|:||:||:|||||||||||||||
Db    522    TGTGCTGCCTCAAAAATACAAGG 544
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```
RESULT 10
AY866300

LOCUS       AY866300               901 bp    DNA     linear   PRI 24-JAN-2005
DEFINITION  Gorilla gorilla microRNA mir-15a and microRNA mir-16-1 genes,
            complete sequence.
ACCESSION   AY866300
VERSION     AY866300.1  GI:57903102
KEYWORDS    .
SOURCE      Gorilla gorilla (gorilla)
ORGANISM    Gorilla gorilla
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Gorilla.
```

REFERENCE   1 (bases 1 to 901)
AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
TITLE   Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
JOURNAL   Cell 120 (1), 21-24 (2005)
PUBMED   15652478
REFERENCE   2 (bases 1 to 901)
AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
TITLE   Direct Submission
JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
            3584 CT, The Netherlands
FEATURES   Location/Qualifiers
     source   1..901
                     /organism="Gorilla gorilla"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9593"
     misc_RNA   462..544
                     /product="precursor microRNA mir-15a"
                     /note="based on Homo sapiens mir-15a"
     misc_RNA   475..496
                     /product="microRNA mir-15a"
     misc_RNA   602..690
                     /product="precursor microRNA mir-16-1"
                     /note="based on Homo sapiens mir-16-1"
     misc_RNA   615..636
                     /product="microRNA mir-16-1"
ORIGIN

Query Match   100.0%; Score 83; DB 5; Length 901;
Best Local Similarity   73.5%; Pred. No. 1.6e-20;
Matches   61; Conservative   22; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGUGGAAAAGGUGCAGGCCAUAU 60
              ||:||||||:||:||||||:||||:||:||||:|||:|||::||||||||||||||||:|:|:
Db   462 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGTGGATTTTGAAAAGGTGCAGGCCATAT 521

Qy   61 UGUGCCUGCCUCAAAAAUACAAGG 83
              :|:||:|||:||||||||||||||
Db   522 TGTGCCTGCCTCAAAAATACAAGG 544

RESULT 11
LOCUS   AY866307   902 bp   DNA   linear   PRI 24-JAN-2005
DEFINITION Pan troglodytes microRNA mir-15a and microRNA mir-16-1 genes,
            complete sequence.
ACCESSION   AY866307
VERSION   AY866307.1 GI:57903109
KEYWORDS   .
SOURCE   Pan troglodytes (chimpanzee)
  ORGANISM Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1 (bases 1 to 902)
AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
TITLE   Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
JOURNAL   Cell 120 (1), 21-24 (2005)
PUBMED   15652478
REFERENCE   2 (bases 1 to 902)
AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
TITLE   Direct Submission
JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
            3584 CT, The Netherlands
FEATURES   Location/Qualifiers
     source   1..902
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     misc_RNA   463..545
                     /product="precursor microRNA mir-15a"
                     /note="based on Homo sapiens mir-15a"
     misc_RNA   476..497
                     /product="microRNA mir-15a"
     misc_RNA   603..691
                     /product="precursor microRNA mir-16-1"
                     /note="based on Homo sapiens mir-16-1"
     misc_RNA   616..637
                     /product="microRNA mir-16-1"
ORIGIN

Query Match   100.0%; Score 83; DB 5; Length 902;
Best Local Similarity   73.5%; Pred. No. 1.6e-20;
Matches   61; Conservative   22; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGUGGAAAAGGUGCAGGCCAUAU 60
              ||:||||||:||:||||||:||||:||:||||:|||:|||::||||||||||||||||:|:|:
Db   463 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGTGGATTTTGAAAAGGTGCAGGCCATAT 522

Qy   61 UGUGCCUGCCUCAAAAAUACAAGG 83
              :|:||:|||:||||||||||||||
Db   523 TGTGCCTGCCTCAAAAATACAAGG 545

RESULT 12
LOCUS   AY866303   914 bp   DNA   linear   PRI 24-JAN-2005
DEFINITION Pan paniscus microRNA mir-15a and microRNA mir-16-1 genes, complete
            sequence.
ACCESSION   AY866303
VERSION   AY866303.1 GI:57903105
KEYWORDS   .
SOURCE   Pan paniscus (pygmy chimpanzee)
  ORGANISM Pan paniscus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1 (bases 1 to 914)
AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
TITLE   Phylogenetic Shadowing and Computational Identification of Human
            microRNA Genes
JOURNAL   Cell 120 (1), 21-24 (2005)
PUBMED   15652478
REFERENCE   2 (bases 1 to 914)
AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H. and Cuppen,E.
TITLE   Direct Submission
JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
            3584 CT, The Netherlands
FEATURES   Location/Qualifiers
     source   1..914
                     /organism="Pan paniscus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9597"
     misc_RNA   475..557
                     /product="precursor microRNA mir-15a"
                     /note="based on Homo sapiens mir-15a"
     misc_RNA   488..509
                     /product="microRNA mir-15a"
     misc_RNA   615..703
                     /product="precursor microRNA mir-16-1"
                     /note="based on Homo sapiens mir-16-1"
     misc_RNA   628..649
                     /product="microRNA mir-16-1"
ORIGIN

Query Match   100.0%; Score 83; DB 5; Length 914;
Best Local Similarity   73.5%; Pred. No. 1.6e-20;
Matches   61; Conservative   22; Mismatches   0; Indels   0; Gaps   0;

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Qy         1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUGUGAAAAGGUGGCAGGCCAUAU 60
             ||:||||||||||||||||||||||||||||||:||:|||||||||||:|||||||||||:|
Db       475 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTGTGAAAAGGTGCAGGCCATAT 534

Qy        61 UGUGCUGCCUCAAAAAUACAAGG 83
             |:|||||||||:|||:||||||||
Db       535 TGTGCTGCCTCAAAAATACAAGG 557
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RESULT 13

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LOCUS       AC069475/c
DEFINITION  AC069475
            Homo sapiens chromosome 13 clone 317g11 map 13q14, complete
            sequence.
ACCESSION   AC069475
VERSION     AC069475.27  GI:11992970
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 153092)
AUTHORS     Malaj,E., Cowell,J.K. and Roe,B.A.
TITLE       Homo sapiens Chromosome 13q14 BAC Clone 317g11
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 153092)
AUTHORS     Malaj,E., Cowell,J.K. and Roe,B.A.
TITLE       Direct Submission
JOURNAL     Submitted (01-JUN-2000) Department of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   3  (bases 1 to 153092)
AUTHORS     Malaj,E., Cowell,J.K. and Roe,B.A.
TITLE       Direct Submission
JOURNAL     Submitted (27-DEC-2000) Department of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   4  (bases 1 to 153092)
AUTHORS     Malaj,E., Cowell,J.K. and Roe,B.A.
TITLE       Direct Submission
JOURNAL     Submitted (09-APR-2003) Department of Chemistry And Biochemistry,
            The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Dec 27, 2000 this sequence version replaced gi:11560201.
            -------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            --------------
FEATURES             Location/Qualifiers
     source          1..153092
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /clone="317g11"
                     /clone_lib="Scb Research Genetics"
ORIGIN
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Query Match         100.0%;  Score 83;  DB 5;  Length 153092;
Best Local Similarity   73.5%;  Pred. No. 2.2e-20;
Matches    61;  Conservative   22;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUGUGAAAAGGUGGCAGGCCAUAU 60
             ||:||||||||||||||||||||||||||||||:||:|||||||||||:|||||||||||:|
Db       436 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTGTGAAAAGGTGCAGGCCATAT 377

Qy        61 UGUGCUGCCUCAAAAAUACAAGG 83
             |:|||||||||:|||:||||||||
Db       376 TGTGCTGCCTCAAAAATACAAGG 354
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RESULT 14

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LOCUS       AF334404/c                 154868 bp    DNA     linear   PRI 19-APR-2001
DEFINITION  Homo sapiens chromosome 13q14 BAC clone CITB-369L16, complete
            sequence.
ACCESSION   AF334404
VERSION     AF334404.1  GI:13507269
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 154868)
AUTHORS     Mabuchi,H., Fujii,H., Calin,G., Alder,H., Negrini,M., Rassenti,L.,
            Kipps,T.J., Bullrich,F. and Croce,C.M.
TITLE       Cloning and characterization of CLLD6, CLLD7, and CLLD8, novel
            candidate genes for leukemogenesis at chromosome 13q14, a region
            commonly deleted in B-cell chronic lymphocytic leukemia
JOURNAL     Cancer Res. 61 (7), 2870-2877 (2001)
PUBMED      11306461
REFERENCE   2  (bases 1 to 154868)
AUTHORS     Fujii,H., Inoue,H., Alder,H., Negrini,M., Bullrich,F. and
            Croce,C.M.
TITLE       Sequencing of the chromosome 13q14 region deleted in B-CLL
JOURNAL     Unpublished
REFERENCE   3  (bases 1 to 154868)
AUTHORS     Mabuchi,H., Fujii,H., Calin,G., Alder,H., Negrini,M., Bullrich,F.
            and Croce,C.M.
TITLE       Direct Submission
JOURNAL     Submitted (09-JAN-2001) Kimmel Cancer Center, Thomas Jefferson
            Medical College, BLSB, Rm. 1006, 233 S. 10th Street, Philadelphia,
            PA 19107, USA
FEATURES             Location/Qualifiers
     source          1..154868
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="13q14"
                     /clone="CITB-369L16 BAC clone"
     gene            48282..63788
                     /gene="RFP2"
                     /note="LEU5; similar to Homo sapiens candidate tumor
                     suppressor cDNA sequence presented in GenBank Accession
                     Number AJ224819"
     gene            complement(94133..132624)
                     /gene="DLEU2"
                     /note="LEU2; similar to Homo sapiens leukemia associated
                     gene 2 cDNA sequence presented in GenBank Accession Number
                     Y15228"
     gene            132819..>154868
                     /gene="DLEU1"
                     /note="LEU1; similar to Homo sapiens leukemia associated
                     gene 1 cDNA sequence presented in GenBank Accession Number
                     Y15227"
ORIGIN
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Query Match         100.0%;  Score 83;  DB 5;  Length 154868;
Best Local Similarity   73.5%;  Pred. No. 2.2e-20;
Matches    61;  Conservative   22;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUGUGAAAAGGUGGCAGGCCAUAU 60
             ||:||||||||||||||||||||||||||||||:||:|||||||||||:|||||||||||:|
Db     99823 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTGTGAAAAGGTGCAGGCCATAT 99764

Qy        61 UGUGCUGCCUCAAAAAUACAAGG 83
             |:|||||||||:|||:||||||||
Db     99763 TGTGCTGCCTCAAAAATACAAGG 99741
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RESULT 15

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LOCUS       AL137060/c
DEFINITION  AL137060              154887 bp    DNA     linear   PRI 18-MAY-2005
            Human DNA sequence from clone RP11-34F20 on chromosome 13 Contains
            the 3' end of the RFP2 gene for ret finger protein 2, the DLEU2
            gene for deleted in lymphocytic leukemia 2 (LEU2 BCMSUN), the 5'
            end of the DLEU1 gene for deleted in lymphocytic leukemia 1 (BCMS
            LEU1), a ribosomal protein L18 (RPL18) pseudogene, a novel gene and
            four CpG islands, complete sequence.
ACCESSION   AL137060
VERSION     AL137060.13  GI:11120982
KEYWORDS    HTG; BCMS; BCMSUN; CpG island; DLEU1; DLEU2; LEU1; LEU2;
            lymphocytic leukemia; RFP2; RPL18.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 154887)
  AUTHORS   Pearce,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 8, 2000 this sequence version replaced gi:11022355.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 13, constructed by the Sanger Centre Chromosome 13
            Mapping Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr13
            RP11-34F20 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            --------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            ---------------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
FEATURES             Location/Qualifiers
     source          1..154887
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /clone="RP11-34F20"
                     /clone_lib="RPCI-11.1"
     misc_feature    1
                     /note="Clone_left_end: RP11-34F20"
     gene            join(AL391993.20:26230..26230,AL391993.20:26878..26974,
                     5394..7790)
                     /gene="RFP2"
     mRNA            join(AL391993.20:26230..26342,AL391993.20:26878..26974,
                     5394..7790)
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-005"
                     /product="ret finger protein 2"
                     /note="match: ESTs: AI082097 AI174535 AI400465 AI433784
                     AI675587 AL526848 AU117766 AU134155 AU155253
                     AW874522 AW961863 BG054611 BG401428 BI090269 BI183262
                     BI194225 BM563515 BM673398 BM682100 BM811480
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                     BQ011072 BQ018724
     match:          cDNAs: AF220127 AF241850 AK001806 AL360196"
                     join(AL391993.20:26260..26260..26427,AL391993.20:26878..26974,
                     5394..6627)
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-006"
     mRNA            join(AL391993.20:26260..26427,AL391993.20:26878..26974,
                     5394..6627)
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-006"
                     /product="ret finger protein 2"
                     /note="match: ESTs: AL543861 AL583364 BE207206 BE383796
                     BG939137
     match:          cDNAs: BC003579"
                     join(AL391993.20:25714..26061,AL391993.20:26878..26974,
                     5394..6199)
                     /gene="RFP2"
     mRNA            join(AL391993.20:25714..26061,AL391993.20:26878..26974,
                     5394..>6199)
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-007"
                     /product="ret finger protein 2"
                     /note="match: ESTs: BG718270 BG723498 BI462388 BI520507
                     BQ420389"
     gene            join(AL391993.20:25099..25186,AL391993.20:26878..26974,
                     AL391993.20:30206..30319,5394..>5786)
                     /gene="RFP2"
     mRNA            join(AL391993.20:25099..25186,AL391993.20:26878..26974,
                     AL391993.20:30206..30319,5394..>5786)
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-004"
                     /product="ret finger protein 2"
                     /note="match: ESTs: BG718712.1"
     gene            5400..6623
                     /gene="RFP2"
     CDS             5400..>6199
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-005"
                     /standard_name="OTTHUMP00000018431"
                     /codon_start=1
                     /product="ret finger protein 2"
                     /protein_id="CAC43391.1"
                     /db_xref="GI:14594775"
                     /db_xref="GOA:Q60858"
                     /db_xref="HGNC:9976"
                     /db_xref="HSSP:1UM7"
                     /db_xref="InterPro:IPR000315"
                     /db_xref="UniProtKB/Swiss-Prot:O60858"
                     /translation="MELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSVRN
                     SLWRPAPKKCPTCRKETSATGINSLQVNYSLKGIVEKYNKIKISPKMPVCKGHLGQPL
                     NIFCLTDMQLICIGCATRGEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSR
                     LDTLETSRKSLQLLTKDSDKVKFPEFKLQHTDQKNEILSDFETMKLAVMQAYDPE
                     INKLNTILQEQRMAFNIAEAFKDVSEPIVFLQOMQEFREKIKVIKETFLPPSNLPASP
                     LMKNFDTSQWEDIKLVDVDKLSLPQDTGFPISKIPWSFYKLFLLILLGLVIPGPTM
                     FLEWSLPDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIENERFKNFTLV
                     VLNNVAFVCVKYKLL"
     CDS             5400..>6199
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-007"
                     /standard_name="OTTHUMP00000018433"
                     /codon_start=1
                     /product="ret finger protein 2"
                     /protein_id="CAH72826.1"
                     /db_xref="GI:55661782"
                     /db_xref="GOA:Q5W0U8"
                     /db_xref="InterPro:IPR001841"
                     /db_xref="InterPro:IPR001315"
                     /db_xref="UniProtKB/TrEMBL:Q5W0U8"
                     /translation="MELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSVRN
                     SLWRPAPKKCPTCRKETSATGINSLQVNYSLKGIVEKYNKIKISPKMPVCKGHLGQPL
                     NIFCLTDMQLICIGCATRGEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSR
                     LDTLETSRKSLQLLTKDSDKVKFPEFKLQHTDQKNEILSDFETMKLAVMQAYDPE"
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     gene            join(AL391993.20:26260..26260,AL391993.20:26878..26974,
                     5394..7790)
                     /gene="RFP2"
                     /locus_tag="RP11-34F20.3-006"
     mRNA            join(AL391993.20:26260..26427,AL391993.20:26878..26974,
                     5394..6627)
                     /gene="RFP2"
     gene            join(AL391993.20:25099..25186,AL391993.20:26878..26974,
                     AL391993.20:30206..30319,5394..>5786)
                     /gene="RFP2"
     mRNA            join(AL391993.20:25099..25186,AL391993.20:26878..26974,
                     AL391993.20:30206..30319,5394..>5786)
                     /gene="RFP2"
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                INKLNTILQEORWAFNIAEAFKDVSEPIVEPLQQMOEFREKIKVIKETP

CDS             5400. .>5786
                /gene="RFP2"
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                /codon_start=1
                /standard_name="OTTHUMP00000018430"
                /product="ret finger protein 2"
                /protein_id="CAH72825.1"
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                /db_xref="InterPro:IPR000315"
                /db_xref="InterPro:IPR001841"
                /db_xref="UniProtKB/TrEMBL:Q5W0U9"
                /translation="MELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSVRN
                SLWRPAPFKCPTCRKETSATGINSLQVNYSLKGIVEKYNKIKISPKMPVCKGHLGQPL
                NIFCLTDMQLICGICATRGEHTKHVFC"

polyA_signal    6609. .6614
                /gene="RFP2"

polyA_site      6629
                /gene="RFP2"

mRNA            join(8903. .9530,12282. .12379,13673. .14379)
                /gene="RFP2"
                /locus_tag="RP11-34F20.3-006"

gene            join(8903. .9530,12282. .12379,13673. .14379)
                /gene="RFP2"
                /locus_tag="RP11-34F20.3-005"

mRNA            join(8903. .9530,12282. .12379,13673. .14379)
                /gene="RFP2"
                /locus_tag="RP11-34F20.3-002"
                /product="ret finger protein 2"
                /note="match: cDNAs: BC020887"

gene            join(8919. .9530,13673. .13856)
                /gene="RFP2"
                /locus_tag="RP11-34F20.3-003"

mRNA            join(8919. .9530,13673. .13856)
                /gene="RFP2"

gene            join(AL391993.20:26230. .26342,AL391993.20:26878. .26974,
                13673. .13940)
                /gene="RFP2"
                /note="match: ESTs: BI770863"

mRNA            join(AL391993.20:26230. .26342,AL391993.20:26878. .26974,
                13673. .13940)
                /gene="RFP2"
                /locus_tag="RP11-34F20.3-001"
                /product="ret finger protein 2"

gene            join(AL391993.20:26024. .26061,AL391993.20:26878. .26974,
                13673. .13940)
                /gene="RFP2"

mRNA            join(AL391993.20:26024. .26061,AL391993.20:26878. .26974,
                13673. .13940)
                /gene="RFP2"
                /locus_tag="RP11-34F20.3-008"
                /note="match: ESTs: AA815248"
                /product="ret finger protein 2"
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Best Local Similarity   73.5%;   Pred. No. 2.2e-20;
Matches 61;   Conservative 22;   Mismatches 0;   Indels 0;   Gaps 0;

Qy        1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGGUUUGUGGAUUUUGAAAGGUGCAGGCCAUAU 60
            ||::|||||::|||||||||||||::::||:::|:||||||||||||||||||||:||:|:
Db    42660 CCUUGGAGUAAAGUAGCAGCACAUAAUGGGUUUGUGGAUUUUGAAAGGUGCAGGCCAUAU 42601

Qy       61 UGUGCUCGCCCUCAAAAAUACAAGG 83
            :|:||||:|||::||||||||||||
Db    42600 TGTGCTCGCCCTCAAAAATACAAGG 42576
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Search completed: November 1, 2006, 20:59:43
Job time : 1838.86 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioccceleration Ltd.

Run on: November 1, 2006, 19:02:55 ; Search time 397.61 Seconds
(without alignments)
1455.440 Million cell updates/sec

Title: US-10-706-798-1
Perfect score: 83
Sequence: 1 ccuggaguaaguagcagc..........gcugccucaaaauacaagg 83
Searched: 5244920 seqs, 3486124231 residues
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2004as:*
12: geneseqn2004bs:*
13: geneseqn2005as:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	83	12	AD017089	Ado17089 Human miR
2	83	100.0	83	14	AEB92620	Aeb92620 Human mic
3	83	100.0	83	14	AED35990	Aed35990 Human mic
4	83	100.0	83	14	AEE26703	Aee26703 Hsa miR-1
5	83	100.0	83	15	AEE99350	Aee99350 Human miR
6	83	100.0	310	14	ADX03808	Adx03808 Human gen
7	83	100.0	4214	4	AAK72317	Aak72317 Human imm
8	82	98.8	110	14	ADX03045	Adx03045 Human pri
9	80	96.4	110	14	ADX03080	Adx03080 Human pri
10	79	95.2	108	14	AEB92619	Aeb92619 Human mic
11	68.6	82.7	83	15	AEE99543	Aee99543 Mouse miR
12	61.8	74.5	70	14	ADX04205	Adx04205 Mouse pri
13	40	48.2	40	14	AEB92912	Aeb92912 Human mic
14	40	48.2	40	14	AEB92913	Aeb92913 Human mic
15	33.4	40.2	83	12	AD017089	Ado17089 Human miR
16	33.4	40.2	83	14	AEB92620	Aeb92620 Human mic
17	33.4	40.2	83	14	AED35990	Aed35990 Human mic
18	33.4	40.2	83	15	AEE26703	Aee26703 Hsa miR-1
c 19	33.4	40.2	83	15	AEE99350	Aee99350 Human miR
c 20	33.4	40.2	310	14	ADX03808	Adx03808 Human gen
c 21	33.4	40.2	4214	14	AAK72317	Aak72317 Human imm
c 22	32.4	39.0	110	14	ADX03045	Adx03045 Human pri
c 23	32.4	39.0	110	14	ADX03080	Adx03080 Human pri
c 24	30.4	36.6		15	AEE99350	Aee99350 Human miR
c 25	30.4	36.6	30	15	AEF00087	Aef00087 DNA probe
c 26	29.6	35.7	108	14	AEI17143	Aei17143 Mouse S1-
c 27	28.4	34.2	2492	4	AAF61948	Aaf61948 T. thermo
c 28	28.4	33.7	1313	14	AEB67609	Aeb67609 Rice geno
c 29	27.6	33.3	4745	14	AED14812	Aed14812 DNA encod
c 30	27.4	33.0	4940	14	ADX03045	Adx03045 Human CDN
c 31	27.4	33.0	2843	8	ACA23222	Aca23222 Prokaryot
c 32	27.4	33.0	267	14	AAH16588	Aah16588 Leukaemia
c 33	27.4	33.0	4940	10	ADF82143	Adf82143 Leukaemia
c 34	27	33.0	110000	2	AAX20248	Aax20248 Borrelia
c 35	27.2	32.8	110000	10	ADF82144	Adf82144 Leukaemia
c 36	27.2	32.8	98	14	ADX04176	Adx04176 Mouse pri
c 37	27.2	32.8	98	14	AEB92622	Aeb92622 Human mic
c 38	27.2	32.8	98	15	AEE99740	Aee99740 Rat miRNA
c 39	27.2	32.8	110	14	AEE99351	Aee99351 Human miR
c 40	27.2	32.8	66743	4	ABL27118	Abl27118 Drosophil
c 41	27	32.5	27	14	ADX03789	Adx03789 Human pri
c 42	27	32.5	3396	13	ADX47216	Adx47216 Bacterial
c 43	27	32.5	3396	13	ADU00612	Adu00612 Nucleotid
c 44	27	32.5	64125	13	ABD33295	Abd33295 Human can
c 45	27	32.5	96599	10	ADC85298	Adc85298 Human Egr

ALIGNMENTS

RESULT 1
AD017089

ID   AD017089 standard; RNA; 83 BP.
XX
AC   AD017089;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human miR15 precursor RNA sequence SeqID1.
XX
KW   miR15; miR16; cancer; proliferation; cancer cell; cytostatic;
KW   gene therapy; chronic lymphocytic leukaemia; prostate cancer; micro RNA;
KW   chromosome 13q14; human; 88.
XX
OS   Homo sapiens.
OS
XX
FH   Key   Location/Qualifiers
FH
FT   misc_binding   1..5
FT   /*tag= a
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 83-79
FT   misc_binding   16..23
FT   /*tag= b
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 68-61
FT   misc_binding   26..35
FT   /*tag= c
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 58-49
FT   misc_binding   38..40
FT   /*tag= d
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 46-44
FT   misc_binding   44..46
FT   /*tag= e
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 40-38

FT   misc_binding
FT   of itself"
FT   49..58
FT   /*tag= f
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 35-26
FT   misc_binding
FT   of itself"
FT   61..68
FT   /*tag= g
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 23-16
FT   misc_binding
FT   79..83
FT   /*tag= h
FT   /bound_moiety= "Binds to itself"
FT   /note= "Forms a double stranded region with bases 5-1 of
FT   itself"
XX
PN   WO2004043387-A2.
XX
PD   27-MAY-2004.
XX
PF   12-NOV-2003; 2003WO-US035777.
XX
PR   13-NOV-2002; 2002US-0425864P.
PR   09-MAY-2003; 2003US-0469464P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Croce CM, Calin GA;
XX
DR   WPI; 2004-400825/37.
XX
PT   Treating an miR15 or miR16 mediated cancer, comprises administering to the subject an
miR15 or miR16 gene product.
PT   leukemia or prostate cancer, comprises administering to the subject an
XX
PS   Claim 64; SEQ ID NO 1; 73pp; English.
XX

CC   This invention relates to a novel method of treating an miR15 or miR16
mediated cancer in a subject which comprises administering to the subject
an amount of an isolated miR15 or miR16 gene product such that
proliferation of miR15 or miR16 mediated cancer cells in inhibited. The
miR15 and miR16 micro RNA genes are localised to 13q14 in humans, a
region that is deleted in a significant portion of subjects suffering
from chronic lymphocytic leukemia or prostate cancer. The products of
the miR15 and miR16 genes have also been found to inhibit the neoplastic
or tumourigenic growth of chronic lymphocytic leukaemia or prostate
cancer cells. The invention may be useful for the production of compounds
with a cytostatic activity. In addition the invention may also be useful
for gene therapy using the miR15 or miR16 gene product. The methods and
compositions are useful in diagnosing and treating miR15 or miR16
mediated cancer, i.e. chronic lymphocytic leukaemia or prostate cancer.
The present sequence is that of the human miR15 precursor RNA sequence
which is used in the method of the invention.

SQ   Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;

Query Match   100.0%;   Score 83;   DB 12;   Length 83;
Best Local Similarity   100.0%;   Pred. No. 2.1e-20;
Matches 83;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
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Db   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60

Qy 61 UGUGCUGCUCUCAAAAUACAAGG 83
        |||||||||||||||||||||||
Db 61 UGUGCUGCUCUCAAAAUACAAGG 83

RESULT 2
AEB92620
ID   AEB92620 standard; DNA; 83 BP.
XX
AC   AEB92620;
XX
DT   03-NOV-2005 (first entry)
XX
DE   Human microRNA gene SEQ ID NO 33.
XX
KW   cytostatic; gene therapy; diagnosis; prognosis; pharmaceutical;
KW   gene expression; musculoskeletal disease; hematological disease;
KW   immunostimulant; andrology; neurological disease; dermatological disease;
KW   endocrine disease; gynecology and obstetrics; respiratory disease;
KW   gastrointestinal disease; genitourinary disease; cancer; neoplasm;
KW   microRNA; miR; ss; biochip.
XX
OS   Homo sapiens.
XX
PN   WO2005078139-A2.
XX
PD   25-AUG-2005.
XX
PF   09-FEB-2005; 2005WO-US004865.
XX
PR   09-FEB-2004; 2004US-0542929P.
PR   09-FEB-2004; 2004US-0542940P.
PR   09-FEB-2004; 2004US-0542903P.
PR   09-FEB-2004; 2004US-0543119P.
PR   18-JUN-2004; 2004US-0580797P.
PR   18-JUN-2004; 2004US-0580959P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Croce CM, Liu C, Calin GA;
XX
DR   WPI; 2005-571622/58.
XX
PT   Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,
tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in
the test sample.
XX
PS   Example 1; SEQ ID NO 33; 170pp; English.
XX

CC   The invention describes diagnosing whether a subject has, or is at risk
for developing, a cancer linked to a cancer-associated chromosomal
feature, comprises evaluating the status in the subject of at least one
microRNA (miR) gene located in close proximity to the cancer-associated
chromosomal feature. Also described are a pharmaceutical composition
comprising an isolated miR gene product or a nucleic acid encoding an
isolated miR gene product from an miR gene located in close proximity to
a cancer-associated chromosomal feature and is not miR15 or miR16, and a
pharmaceutical carrier; and a method of treating cancer associated with a
cancer-associated chromosomal feature in a subject. The miR, composition,
and method are useful for diagnosing and treating a cancer-associated
chromosomal feature, where the cancer is bladder cancer, esophageal
cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,
ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic
tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,
epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,
head-and-neck cancer, renal cancer, male germ cell tumors, malignant
mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,
prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilm's
tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,
neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid
leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,
medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
associated with an unmutated IgVH gene, ZAP-70 expression, CD38
expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
their combination. This sequence represents a human microRNA (miRNA)
gene.
XX
SQ   Sequence 83 BP; 26 A; 13 C; 22 G; 22 T; 0 U; 0 Other;

Query Match   100.0%;   Score 83;   DB 14;   Length 83;

RESULT 3

Best Local Similarity 73.5%; Pred. No. 2.1e-20; Indels 0; Gaps 0;
Matches 61; Conservative 22; Mismatches 0;

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         ||||||:||||||||||:||:|||||||||||||||||:||||:||:|||||||||:|:
Db    1 CCUUGGAGUAAAAGYAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60

Qy   61 UGUGCUGCCUCAAAAAAUACAAGG 83
         :|:||:||:|||||:||||||||||
Db   61 TGTGCTGCCTCAAAAATACAAGG 83
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ID   AED35990 standard; RNA; 83 BP.
XX
AC   AED35990;
XX
DT   15-DEC-2005 (first entry)
XX
DE   Human micro RNA miR-15a precursor.
XX
KW   RNA interference; RNA purification; RNA amplification; gene silencing;
KW   RNA detection; micro RNA; miRNA; miR-15a; ss.
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   stem_loop   1..83
FT   /*tag= a
FT   misc_RNA   14..35
FT   /*tag= b
FT   /note= "Corresponds to mature miRNA"
XX
PN   WO2005098029-A2.
PD   20-OCT-2005.
XX
DR   WPI; 2005-714540/73.
XX
PA   (EXIQ-) EXIQON AS.
PI   Jacobsen N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;
PI   Nielsen PS, Norholm M;
XX
PR   07-APR-2004; 2004DK-0000578.
PR   23-JUL-2004; 2004DK-0001146.
PR   11-AUG-2004; 2004DK-0001218.
PR   15-OCT-2004; 2004DK-0001587.
PR   28-JAN-2005; 2005DK-0000140.
PT   Isolating, purifying, amplifying, detecting, identifying, quantifying or
PT   capturing non-coding RNAs such as micro RNA or small interfering RNA
PT   (siRNA), involves using oligonucleotide containing nucleoside analogs.
XX
PS   Disclosure; Fig 29; 180pp; English.

CC   The present invention relates to the use of an oligonucleotide for the
CC   isolation, purification, amplification, detection, identification,
CC   quantitation or capture of microRNA (miRNA) or small interfering RNA
CC   (siRNA), where the oligonucleotide contains a number of nucleoside
CC   analogs. The method uses 2 anchored tagging probes, each designed in
CC   combination to detect a complementary target sequence, e.g. a short RNA
CC   sequence, where the first tagging probe hybridizes to a first region
CC   within a target sequence and the second tagging probe hybridizes to a
CC   second region within the same complementary target sequence, e.g. a short
CC   RNA target sequence that is adjacent to the first region. In a preferred
CC   mode, one of the tagging probes is 5' phosphorylated to enable covalent
CC   coupling of the 2 contiguous tagging probes hybridized to the
CC   complementary target sequence by a ligase to form a single
CC   oligonucleotide sequence. The method takes advantage of substitution of

---

CC   the recognition sequences with high-affinity nucleotide analogs, e.g.
CC   locked nucleic acid (LNA), for sensitive and specific hybridization to
CC   short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is
CC   followed by real-time quantitative PCR (qPCR) of the target sequence,
CC   e.g. ribonucleic acid-templated, covalently joined oligonucleotide
CC   molecules using anchor sequences attached to the tagging probes as
CC   priming sites for the PCR primers and a short detection probe with
CC   sufficient duplex stability to allow binding to the amplicon, and
CC   employing any of a variety of detection principles used in homogeneous
CC   assays. In the preferred mode, the detection probe is substituted with
CC   duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and
CC   preferably oxy-LNA, to allow the use of short detection probes in the
CC   real-time qPCR. The method is useful for detecting and quantifying
CC   individual small RNA molecules in complex mixtures of different nucleic
CC   acids, and for detecting, testing, diagnosing or quantifying miRNAs,
CC   siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA
CC   splice variants implicated in, or connected to, human disease in complex
CC   nucleic acid samples, e.g. from cancer patients. The present sequence is
CC   that of human miRNA Hsa miR-15a precursor. miR-15a AED35991 was used as
CC   the target in examples from the invention.
XX
SQ   Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;

Query Match   100.0%; Score 83; DB 14; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
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Db    1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60

Qy   61 UGUGCUGCCUCAAAAAAUACAAGG 83
         ||||||||||||||||||||||||
Db   61 UGUGCUGCCUCAAAAAAUACAAGG 83
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RESULT 4

ID   AEE26703 standard; RNA; 83 BP.
XX
AC   AEE26703;
XX
DT   09-FEB-2006 (first entry)
XX
DE   Hsa miR-15a precursor sequence, SEQ ID 72.
XX
KW   RNA amplification; RNA detection; RNA purification; miRNA; microRNA; ss.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   misc_binding   1..5
FT   /*tag= a
FT   /bound_moiety= "Nucleotides 83..79 of the present
FT   sequence"
FT   misc_binding   13
FT   /*tag= b
FT   /bound_moiety= "Nucleotide 71 of the present sequence"
FT   misc_binding   16..23
FT   /*tag= c
FT   /bound_moiety= "Nucleotides 68..61 of the present
FT   sequence"
FT   misc_binding   26..35
FT   /*tag= d
FT   /bound_moiety= "Nucleotides 58..49 of the present
FT   sequence"
FT   misc_binding   38..39
FT   /*tag= e
FT   /bound_moiety= "Nucleotides 46..45 of the present
FT   sequence"
FT   misc_binding   45..46
FT   /*tag= f
FT   /bound_moiety= "Nucleotides 39..38 of the present
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RESULT 5
'AEE99350

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FT   misc_binding   49..58
FT                  /*tag= g
FT                  /bound_moiety= "Nucleotides 35..26 of the present
FT                  sequence"
FT   misc_binding   61..68
FT                  /*tag= h
FT                  /bound_moiety= "Nucleotides 23..16 of the present
FT                  sequence"
FT   misc_binding   71
FT                  /*tag= i
FT                  /bound_moiety= "Nucleotide 13 of the present sequence"
FT   misc_binding   79..83
FT                  /*tag= j
FT                  /bound_moiety= "Nucleotides 5..1 of the present sequence"
XX
PN   US20052272075-A1.
XX
PD   08-DEC-2005.
XX
PF   07-APR-2005; 2005US-00100897.
XX
PR   28-JAN-2005; 2005US-0648221P.
PR   15-OCT-2004; 2004US-0619291P.
PR   12-AUG-2004; 2004US-0600961P.
PR   23-JUL-2004; 2004US-0590856P.
PR   07-APR-2004; 2004US-0560148P.
XX
PA   (NORH/) NORHOLM M.
PA   (NIEL/) NIELSEN P S.
PA   (MOUR/) MOURITZEN P.
PA   (ECHW/) ECHWALD S M.
PA   (KAUP/) KAUPPINEN S.
PA   (KONG/) KONGSBAK L.
PA   (JACO/) JACOBSEN N.
XX
PI   Jacobsen N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;
PI   Nielsen PS, Norholm M;
XX
DR   WPI; 2006-037202/04.
XX
PT   Isolating, purifying, amplifying, detecting identifying, quantifying, or
PT   (siRNA) by using an oligonucleotide containing a number of nucleoside
PT   analogues.
XX
PS   Disclosure; SEQ ID NO 72; 111pp; English.
XX
CC   The present invention relates to novel methods for quantifying non-coding
CC   RNAs, such as microRNA or short interfering RNA (siRNA). The methods
CC   comprises using an oligonucleotide containing a number of nucleoside
CC   analogues e.g LNA analogues. The methods are useful for detecting and
CC   quantifying individual small RNA molecules in complex mixtures composed
CC   or hundreds of thousands of different nucleic acids. The present sequence
CC   was used to illustrate the invention.
XX
SQ   Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;

Query Match             100.0%;  Score 83;  DB 15;  Length 83;
Best Local Similarity   100.0%;  Pred. No. 2.1e-20;
Matches   83;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGUGAAAAGGUGCAGGCCAUAU 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGUGAAAAGGUGCAGGCCAUAU 60

Qy         61 UGUGCUGCCUCAAAAAAUACAAGG 83
              ||||||||||||||||||||||||
Db         61 UGUGCUGCCUCAAAAAAUACAAGG 83
```

```
ID   AEE99350 standard; RNA; 83 BP.
XX
AC   AEE99350;
XX
DT   23-FEB-2006  (first entry)
XX
DE   Human miRNA sequence, hsa-mir-15a.
XX
KW   RNA detection; microarray; diagnosis; genetic marker; drug screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200511886-A2.
XX
PD   15-DEC-2005.
XX
PF   31-MAY-2004; 2005WO-US018826.
XX
PR   28-MAY-2004; 2004US-0575743P.
PR   03-FEB-2005; 2005US-0649584P.
XX
PA   (AMBI-) AMBION INC.
XX
PI   Brown D, Conrad R, Devroe E, Goldrick M, Keiger K, Labourier E;
PI   Moon I, Powers P, Shelton J, Shingara J;
XX
DR   WPI; 2006-047544/05.
XX
PS   Disclosure; SEQ ID NO 22; 307pp; English.
XX
CC   The new invention relates to manipulation of miRNA and their use in
CC   characterizing their role and function in cells. Described is a method of
CC   multi-labeling miRNA in a sample by forming a reaction mixture for enzyme
CC   catalysis, comprising the miRNA with an enzyme that catalyzes the
CC   addition of di- or tri-phosphate nucleotides, and one or more labeled or
CC   unlabeled nucleotides, where tailed miRNA molecules are produced; and
CC   attaching a label to the tailed miRNA molecules. Specifically, the method
CC   comprises enriching miRNA in the sample; forming a reaction mixture,
CC   under conditions that allows enzyme catalysis, where tailed miRNA
CC   molecules are produced; and if unlabeled nucleotides are added to the
CC   miRNA, attaching a label to the tailed miRNA molecules. Also given
CC   include a miRNA array comprising one or more miRNA probes immobilized on
CC   a solid support, where the probes comprise an miRNA coding sequence, and
CC   an amine attached to the 5' or 3' end of the probe; evaluating miRNA in a
CC   sample; identifying a correlation between miRNA expression and a disease
CC   or condition; analyzing miRNA in a sample; identifying a candidate
CC   diagnostic marker or therapeutic target of a disease or condition;
CC   determining a difference between two or more biological samples;
CC   screening for a candidate therapeutic agent for a disease or condition;
CC   and a kit for preparing miRNA for multi-labeling. The methods and
CC   compositions are useful for isolating, enriching, and/or labeling miRNA
CC   molecule samples. The present sequence is a human miRNA sequence, used in
CC   the new methods of the invention.
XX
PT   Multi-labeling miRNA in a sample, by forming a reaction mixture for
PT   enzyme catalysis, where tailed miRNA molecules are produced, and
PT   attaching a label to the tailed miRNA molecules.
XX
SQ   Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;

Query Match             100.0%;  Score 83;  DB 15;  Length 83;
Best Local Similarity   100.0%;  Pred. No. 2.1e-20;
Matches   83;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGUGAAAAGGUGCAGGCCAUAU 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGUGAAAAGGUGCAGGCCAUAU 60

Qy         61 UGUGCUGCCUCAAAAAAUACAAGG 83
              ||||||||||||||||||||||||
Db         61 UGUGCUGCCUCAAAAAAUACAAGG 83
```

```
RESULT 6
ID    ADX03808 standard; DNA; 310 BP.
XX
AC    ADX03808;
XX
DT    05-MAY-2005 (first entry)
XX
DE    Human genomic DNA encoding pri-miRNA mir-15a.
XX
KW    MicroRNA; ds; RNA interference; gene silencing; Cytostatic; Antidiabetic;
KW    Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
KW    Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW    Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW    angiogenesis disorder; cardiovascular disease; endocrine disease;
KW    non-insulin dependent diabetes; metabolic disorder; obesity;
KW    gastrointestinal disease; hyperlipidemia; atherosclerosis; atherogenesis;
KW    nutritional disorder; anorexia nervosa; nutritional disorder;
KW    hypertension; anorexia nervosa; nutritional disorder;
KW    psychiatric disorder; Alzheimers disease; degeneration;
KW    neurological disease; nervous system injury; neurodegenerative disease;
KW    neurological disorder.
OS    Homo sapiens.
XX
PN    WO2005013901-A2.
XX
PD    17-FEB-2005.
XX
PF    30-JUL-2004; 2004WO-US025300.
PR    31-JUL-2003; 2003US-0492056P.
PR    31-OCT-2003; 2003US-0516303P.
PR    19-DEC-2003; 2003US-0531596P.
PR    14-APR-2004; 2004US-0562417P.
XX
PA    (ISIS-) ISIS PHARM INC.
XX
PI    Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF;
PI    Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;
PI    Peralta E;
XX
DR    WPI; 2005-163123/17.
XX
PT    New oligomeric compound that can hybridize with or sterically interfere
PT    with nucleic acid molecules comprising or encoding small non-coding RNA
PT    targets, useful for treating e.g. cancer and diabetes.
XX
PS    Example 28; SEQ ID NO 906; 854pp; English.
XX
CC    The invention relates to an oligomeric compound comprising a first region
CC    and a second region, where at least one region contains a modification,
CC    and a portion of the oligomeric compound is targeted to a small non-
CC    coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC    precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC    comprising a first oligomeric compound and a second oligomeric compound
CC    (where at least one of the oligomeric compounds contains a modification,
CC    at least a portion of the first oligomeric compound is capable of
CC    hybridizing with at least a portion of the second oligomeric compound,
CC    and at least a portion of the first oligomeric compound is targeted to a
CC    small non-coding RNA target nucleic acid), a pharmaceutical composition
CC    comprising the composition cited above (and a carrier), a kit or assay
CC    device comprising the composition, modulating the expression of a small
CC    non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC    treating or preventing a disease or disorder associated with a small non-
CC    coding RNA target nucleic acid, treating a condition in an animal,
CC    treating or preventing a disease or disorder associated with CD36,
CC    methods of screening an oligomeric compound for an effect on miRNA
CC    signaling, methods of modulating translation (or apoptosis, conversion of
CC    a precursor miRNA into miRNA, or cellular differentiation), identifying
CC    an RNA transcript bound to a cell at the G2/M phase, interfering with chromosome
CC    delaying) entry of a cell at the small non-coding RNA, interfering with chromosome
CC    segregation, a method of triggering apoptosis, detecting a miRNA
CC    precursor, identifying a miRNA target, modulating cellular
CC    differentiation, treating a condition associated with adipocyte
CC    differentiation in an animal, treating/preventing a disease/disorder
CC    associated with aberrant regulation of the cell cycle by miRNAs,
CC    maintaining a pluripotent stem cell and identifying a small non-coding
CC    RNA binding site. The oligomeric compound is targeted to a region
CC    flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC    increase in expression of a pri-miRNA. The compounds and compositions are
CC    useful for treating a disease or disorder resulting from chromosomal non-
CC    disjunction, altered methylation, acetylation, or pseudouridylation
CC    of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC    neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC    hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia,
CC    Alzheimer's disease, a central nervous system injury or neurodegenerative
CC    disorder. The present sequence is a DNA encoding a primary miRNA of the
CC    invention.
XX
SQ    Sequence 310 BP; 104 A; 41 C; 53 G; 112 T; 0 U; 0 Other;

Query Match       100.0%;  Score 83;  DB 14;  Length 310;
Best Local Similarity   73.5%;  Pred. No. 3.2e-20;
Matches 61;  Conservative 22;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1  CCUUGGAGUAAAGUACGCAGCACAUAAUGUUUGUGUGGAUUUUGAAAAGGUGCAGGCCAUAU  60
          ||:||||||||||||||||||||||||||||||:||::||:|||||||||||||||||||:
Db   131  CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTTGAAAAGGTGCAGGCCATAT  190

Qy    61  UGUGCUGCCUCAAAAAUACAAGG  83
          ||:||||:|||||||||||||||
Db   191  TGTGCTGCCTCAAAAAATACAAGG  213


RESULT 7
AAK72317
ID    AAK72317 standard; DNA; 4214 BP.
XX
AC    AAK72317;
XX
DT    06-NOV-2001 (first entry)
XX
DE    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27129.
XX
KW    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW    cytostatic; gene therapy; vaccine; metastasis; ds.
OS    Homo sapiens.
XX
PN    WO200157182-A2.
XX
PD    09-AUG-2001.
XX
PF    17-JAN-2001; 2001WO-US001354.
PR    31-JAN-2000; 2000US-0179065P.
PR    04-FEB-2000; 2000US-0180828P.
PR    24-FEB-2000; 2000US-0184664P.
PR    02-MAR-2000; 2000US-0186350P.
PR    16-MAR-2000; 2000US-0189874P.
PR    17-MAR-2000; 2000US-0190076P.
PR    18-APR-2000; 2000US-0198123P.
PR    19-MAY-2000; 2000US-0205515P.
PR    07-JUN-2000; 2000US-0204667P.
PR    28-JUN-2000; 2000US-0214886P.
PR    30-JUN-2000; 2000US-0215135P.
PR    07-JUL-2000; 2000US-0216647P.
PR    07-JUL-2000; 2000US-0216680P.
PR    11-JUL-2000; 2000US-0217487P.
PR    11-JUL-2000; 2000US-0217496P.
PR    14-JUL-2000; 2000US-0218290P.
PR    26-JUL-2000; 2000US-0220963P.
PR    26-JUL-2000; 2000US-0220964P.
PR    14-AUG-2000; 2000US-0224518P.
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PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0257577P.
PR   14-AUG-2000; 2000US-0225758P.
PR   23-AUG-2000; 2000US-0271182P.
PR   22-AUG-2000; 2000US-0257759P.
PR   18-AUG-2000; 2000US-0262279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   30-AUG-2000; 2000US-0270009P.
PR   01-SEP-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   06-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0204377P.
PR   08-SEP-2000; 2000US-0211413P.
PR   08-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0211414P.
PR   08-SEP-2000; 2000US-0211243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0232081P.
PR   08-SEP-2000; 2000US-0232080P.
PR   12-SEP-2000; 2000US-0219698P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232298P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   14-SEP-2000; 2000US-0232399P.
PR   21-SEP-2000; 2000US-0242223P.
PR   21-SEP-2000; 2000US-0242274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0270040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240906P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   20-OCT-2000; 2000US-0241809P.
PR   01-NOV-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0244674P.
PR   08-NOV-2000; 2000US-0244675P.
PR   08-NOV-2000; 2000US-0264476P.
PR   08-NOV-2000; 2000US-0246477P.

PR   08-NOV-2000; 2000US-0246478P.
PR   08-NOV-2000; 2000US-0246523P.
PR   08-NOV-2000; 2000US-0245524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0245527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
PR   08-NOV-2000; 2000US-0246609P.
PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   08-NOV-2000; 2000US-0246613P.
PR   17-NOV-2000; 2000US-0249207P.
PR   17-NOV-2000; 2000US-0249208P.
PR   17-NOV-2000; 2000US-0249209P.
PR   17-NOV-2000; 2000US-0249211P.
PR   17-NOV-2000; 2000US-0249212P.
PR   17-NOV-2000; 2000US-0249213P.
PR   17-NOV-2000; 2000US-0249214P.
PR   17-NOV-2000; 2000US-0249215P.
PR   17-NOV-2000; 2000US-0249216P.
PR   17-NOV-2000; 2000US-0249217P.
PR   17-NOV-2000; 2000US-0249218P.
PR   17-NOV-2000; 2000US-0249244P.
PR   17-NOV-2000; 2000US-0249245P.
PR   17-NOV-2000; 2000US-0249264P.
PR   17-NOV-2000; 2000US-0249265P.
PR   17-NOV-2000; 2000US-0249299P.
PR   17-NOV-2000; 2000US-0249300P.
PR   01-DEC-2000; 2000US-0250160P.
PR   01-DEC-2000; 2000US-0250391P.
PR   06-DEC-2000; 2000US-0251479P.
PR   05-DEC-2000; 2000US-0256719P.
PR   05-DEC-2000; 2000US-0251988P.
PR   08-DEC-2000; 2000US-0251030P.
PR   08-DEC-2000; 2000US-0251556P.
PR   08-DEC-2000; 2000US-0251868P.
PR   08-DEC-2000; 2000US-0251869P.
PR   08-DEC-2000; 2000US-0251989P.
PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.

PS   Disclosure; SEQ ID NO 27129; 3071pp + Sequence Listing; English.

PT   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and metastasis.

DR   WPI; 2001-483426/52.

PI   Rosen CA, Barash SC, Ruben SM;

PA   (HUMA-) HUMAN GENOME SCI INC.

CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting the
CC   nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic related diseases, especially
CC   cancers and cancer metastases of haematopoietic antigen genomic
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention

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XX
SQ   Sequence 4214 BP; 1348 A; 698 C; 1374 G; 794 T; 0 U; 0 Other;

Qy   Query Match        100.0%;  Score 83;  DB 4;  Pred. No. 7.8e-20;  Length 4214;
     Best Local Similarity  73.5%;  Conservative 22;  Mismatches 0;  Indels 0;  Gaps 0;
Matches  61;  Conservative 22;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 CCUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
          ||:|||||:||:||||:||||||||||||||||:||::||||||||||||||||||||
Db   2816 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTTGAAAAGGTGCAGGCCATAT 2875

Qy     61 UGUGCUGCCUCAAAAAUACAAGG 83
          :||:||||||||||:||||||||
Db   2876 TGTGCTGCCTCAAAAATACAAGG 2898
XX
Db   2816
Qy     61 UGUGCUGCCUCAAAAAUACAAGG 83
XX

RESULT 8
ID   ADX03045 standard; RNA; 110 BP.
XX
AC   ADX03045;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human primary microRNA (pri-miRNA) mir-15a-1.
XX
KW   MicroRNA; ds; RNA interference; gene silencing; Cytostatic; Antidiabetic;
KW   Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
KW   Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW   Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW   angiogenesis disorder; cardiovascular disease;
KW   non-insulin dependent diabetes; endocrine disease;
KW   gastrointestinal disease; metabolic disorder; obesity;
KW   nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
KW   hypertension; anorexia nervosa; nutritional disorder;
KW   psychiatric disorder; Alzheimers disease; degeneration;
KW   neurological disease; nervous system injury; neurodegenerative disease;
KW   neurological disorder.
XX
OS   Homo sapiens.
XX
PN   WO2005013901-A2.
XX
PD   17-FEB-2005.
XX
PF   30-JUL-2004; 2004WO-US025300.
XX
PR   31-JUL-2003; 2003US-0492056P.
PR   31-OCT-2003; 2003US-0516303P.
PR   19-DEC-2003; 2003US-0531596P.
PR   14-APR-2004; 2004US-0562417P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ebau C, Lollo B, Freier SM, Griffey RH, Baker BF;
PI   Vickers T, Bennett CF, Preier SM, Griffey RH, Baker BF;
PI   Peralta E;
XX
DR   WPI; 2005-163123/17.
XX
PT   New oligomeric compound that can hybridize with or sterically interfere
PT   with nucleic acid molecules comprising or encoding small non-coding RNA
PT   targets, useful for treating e.g., cancer and diabetes.
XX
PS   Example 3; SEQ ID NO 128; 85pp; English.
CC
CC   The invention relates to an oligomeric compound comprising a first region
CC   and a second region, where at least one region contains a modification,
CC   and a portion of the oligomeric compound is targeted to a small non-
CC   coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC   precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC   comprising a first oligomeric compound and a second oligomeric compound
CC   (where at least one of the oligomeric compounds contains a modification,
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CC   at least a portion of the first oligomeric compound is capable of
CC   hybridizing with at least a portion of the second oligomeric compound,
CC   and at least a portion of the first oligomeric compound is targeted to a
CC   small non-coding RNA target nucleic acid), a pharmaceutical composition
CC   comprising the composition cited above (and a carrier), a kit or assay
CC   device comprising the composition, modulating the expression of a small
CC   non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC   treating or preventing a disease or disorder associated with a small non-
CC   coding RNA target nucleic acid, treating a condition in an animal,
CC   treating or preventing a disease or disorder associated with CD36,
CC   methods of screening an oligomeric compound for an effect on miRNA
CC   signaling, methods of screening a miRNA precursor for an effect in miRNA
CC   signaling, methods of modulating translation (or apoptosis, conversion of
CC   a precursor miRNA into miRNA, or cellular differentiation), identifying
CC   an RNA transcript bound to a small non-coding RNA, arresting (or
CC   delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC   segregation, a method of triggering apoptosis, detecting a miRNA
CC   precursor, identifying a miRNA target, modulating cellular
CC   differentiation, treating a condition associated with adipocyte
CC   differentiation in an animal, treating/preventing a disease/disorder
CC   associated with aberrant regulation of the cell cycle by miRNAs,
CC   maintaining a pluripotent stem cell and identifying a small non-coding
CC   RNA binding site. The oligomeric compound is targeted to a region
CC   flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC   increase in expression of a pri-miRNA. The compounds and compositions are
CC   useful for treating a disease or disorder resulting from chromosomal non-
CC   disjunction, altered methylation, acetylation, or pseudouridylation state
CC   of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC   neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC   hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia,
CC   Alzheimer's disease, a central nervous system injury or neurodegenerative
CC   disorder. The present sequence is a primary miRNA of the invention.
XX
SQ   Sequence 110 BP; 40 A; 15 C; 26 G; 0 T; 29 U; 0 Other;

Qy   Query Match        98.8%;  Score 82;  DB 14;  Pred. No. 5.3e-20;  Length 110;
     Best Local Similarity  100.0%;  Pred. No. 5.3e-20;  Length 110;
Matches  82;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 CCUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 CCUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 88

Qy     61 UGUGCUGCCUCAAAAAUACAAG 82
          ||||||||||||||||||||||
Db     89 UGUGCUGCCUCAAAAAUACAAG 110
XX

RESULT 9
ID   ADX03080 standard; RNA; 110 BP.
XX
AC   ADX03080;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human primary microRNA (pri-miRNA) mir-15a-2.
XX
KW   MicroRNA; ds; RNA interference; gene silencing; Cytostatic; Antidiabetic;
KW   Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
KW   Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW   Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW   angiogenesis disorder; cardiovascular disease;
KW   non-insulin dependent diabetes; endocrine disease;
KW   gastrointestinal disease; metabolic disorder; obesity;
KW   nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
KW   hypertension; anorexia nervosa; nutritional disorder;
KW   psychiatric disorder; Alzheimers disease; degeneration;
KW   neurological disease; nervous system injury; neurodegenerative disease;
KW   neurological disorder.
XX
OS   Homo sapiens.
XX
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PN   WO2005013901-A2.

XX

PD   17-FEB-2005.

XX

PF   30-JUL-2004; 2004WO-US025300.

XX

PR   31-JUL-2003; 2003US-0492056P.
PR   31-OCT-2003; 2003US-0516303P.
PR   19-DEC-2003; 2003US-0531596P.
PR   14-APR-2004; 2004US-0562417P.

XX

PA   (ISIS-) ISIS PHARM INC.

XX

PI   Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF;
PI   Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;
PI   Peralta E;

XX

DR   WPI; 2005-163123/17.

XX

PT   New oligomeric compound that can hybridize with or sterically interfere
PT   with nucleic acid molecules comprising or encoding small non-coding RNA
PT   targets, useful for treating e.g., cancer and diabetes.

XX

PS   Example 3; SEQ ID NO 165; 854pp; English.

XX

CC   The invention relates to an oligomeric compound comprising a first region
CC   and a second region, where at least one region contains a modification,
CC   and a portion of the oligomeric compound is targeted to a small non-
CC   coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC   precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC   comprising a first oligomeric compound and a second oligomeric compound
CC   (where at least one of the oligomeric compounds is capable of
CC   at least a portion of the first oligomeric compound is a modification,
CC   hybridizing with at least a portion of the second oligomeric compound,
CC   and at least a portion of the first oligomeric compound is targeted to a
CC   small non-coding RNA target nucleic acid), a pharmaceutical composition
CC   comprising the composition cited above (and a carrier), a kit or assay
CC   device comprising the composition, modulating the expression of a small
CC   non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC   treating or preventing a disease or disorder associated with a small non-
CC   coding RNA target nucleic acid, treating a condition in an animal,
CC   treating or preventing a disease or disorder associated with CD36,
CC   methods of screening an oligomeric compound for an effect on miRNA
CC   signaling, methods of screening a disease or disorder associated with a
CC   precursor miRNA into miRNA, or cellular differentiation), identifying
CC   a precursor miRNA into miRNA, or cellular differentiation), identifying
CC   an RNA transcript bound to a small non-coding RNA, arresting (or
CC   delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC   segregation) entry of a cell at the G2/M phase, interfering with chromosome
CC   precursor, identifying a miRNA target, modulating cellular
CC   differentiation, treating a condition associated with adipocyte
CC   differentiation in an animal, treating/preventing a disease/disorder
CC   associated with aberrant regulation of the cell cycle by miRNAs,
CC   maintaining a pluripotent stem cell and identifying a small non-coding
CC   RNA binding site. The oligomeric compound is targeted to a region
CC   flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC   increase in expression of a pri-miRNA. The compounds and compositions are
CC   useful for treating a disease or disorder resulting from chromosomal non-
CC   disjunction, altered methylation, acetylation, or pseudouridylation state
CC   of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC   neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC   hyperlipidemia, atherosclerosis, hypertension, anorexia,
CC   Alzheimer's disease, a central nervous system injury or neurodegenerative
CC   disorder. The present sequence is a primary miRNA of the invention.

XX

SQ   Sequence 110 BP; 39 A; 15 C; 27 G; 0 T; 29 U; 0 Other;

Query Match   96.4%; Score 80; DB 14; Length 110;
Best Local Similarity   100.0%; Pred. No. 2.9e-19;
Matches 80; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAAGUAGCAGCACAUAAAUGGUUUGUGGAUUUGUGAAAAGGUGCAGGCCAUAU 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   31 CCUUGGAGUAAAAGUAGCAGCACAUAAAUGGUUUGUGGAUUUGUGAAAAGGUGCAGGCCAUAU 90

Qy   61 UGUGCUGCCUCAAAAAUACA 80
               ||||||||||||||||||||
Db   91 UGUGCUGCCUCAAAAAUACA 110

RESULT 10

ID   AEB92619 standard; DNA; 108 BP.

XX

AC   AEB92619;

XX

DT   03-NOV-2005 (first entry)

XX

PN   WO2005078139-A2.

XX

PD   25-AUG-2005.

XX

OS   Homo sapiens.

XX

DE   Human microRNA gene SEQ ID NO 32.

XX

KW   cytostatic; gene therapy; diagnosis; prognosis; pharmaceutical;
KW   gene expression; immunostimulant; musculoskeletal disease; hematological disease;
KW   immunostimulant; andrology; neurological disease; dermatological disease;
KW   endocrine disease; gynecology and obstetrics; respiratory disease;
KW   gastrointestinal disease; genitourinary disease; cancer; neoplasm;
KW   microRNA; miR; ss; biochip.

XX

OS   Homo sapiens.

XX

FH

PF   09-FEB-2005; 2005WO-US004865.

XX

PR   09-FEB-2004; 2004US-0542929P.
PR   09-FEB-2004; 2004US-0542940P.
PR   09-FEB-2004; 2004US-0542963P.
PR   09-FEB-2004; 2004US-0543119P.
PR   18-JUN-2004; 2004US-0580797P.
PR   18-JUN-2004; 2004US-0580959P.

XX

PA   (UYJE-) UNIV JEFFERSON THOMAS.

XX

PI   Croce CM, Liu C, Calin GA;

XX

DR   WPI; 2005-571622/58.

XX

PT   Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,
PT   tumor, or myelodysplastic syndrome, comprises evaluating a miR gene in
PT   the test sample.

XX

PS   Example 1; SEQ ID NO 32; 170pp; English.

XX

CC   The invention describes diagnosing whether a subject has, or is at risk
CC   for developing, a cancer linked to a cancer-associated chromosomal
CC   feature, comprises evaluating the status in the subject of at least one
CC   microRNA (miR) gene located in close proximity to the cancer-associated
CC   chromosomal feature. Also described are a pharmaceutical composition
CC   comprising an isolated miR gene product or a nucleic acid encoding an
CC   isolated miR gene product from an miR gene located in close proximity to
CC   a cancer-associated chromosomal feature and is not miR5 or miR16, and a
CC   pharmaceutical carrier; and a method of treating cancer associated with a
CC   cancer-associated chromosomal feature in a subject. The miR, composition,
CC   and method are useful for diagnosing and treating a cancer-associated
CC   chromosomal feature, where the cancer is bladder cancer, esophageal
CC   cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,
CC   ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic
CC   tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,
CC   epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,
CC   head-and-neck cancer, renal cancer, male germ cell tumors, malignant
CC   mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,
CC   prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilm's
CC   tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,
CC   neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid
CC   leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,

```
CC   medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
CC   chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
CC   associated with an unmutated IgVH gene, ZAP-70 expression, CD38
CC   expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
CC   their combination. This sequence represents a human microRNA (miRNA)
CC   gene.
XX
SQ   Sequence 108 BP; 38 A; 15 C; 26 G; 29 T; 0 U; 0 Other;

Query Match             95.2%;  Score 79;  DB 14;  Length 108;
Best Local Similarity   72.2%;  Pred. No. 6.7e-19;
Matches 57;  Conservative 22;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
        |:||:||||||||||||||||::||:|||||||||||::|||||||::||||:||||:|:|:
Db  30 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 89

Qy  61 UGUGCUGCCUCAAAAAUAC 79
        :||:|||:||||||||||
Db  90 TGTGCTGCCTCAAAAATAC 108


RESULT 11
AEE99543
ID   AEE99543 standard; RNA; 83 BP.
XX
AC   AEE99543;
XX
DT   23-FEB-2006  (first entry)
XX
DE   Mouse miRNA sequence, mmu-mir-15a.
XX
KW   RNA detection; microarray; diagnosis; genetic marker; drug screening; ss.
XX
OS   Mus musculus.
XX
PN   WO200518806-A2.
XX
PD   15-DEC-2005.
XX
PF   31-MAY-2005; 2005WO-US018826.
XX
PR   28-MAY-2004; 2004US-0575743P.
PR   03-FEB-2005; 2005US-0649584P.
XX
PA   (AMBI-) AMBION INC.
XX
PI   Brown D, Conrad R, Devroe E, Goldrick M, Keiger K, Labourier E;
PI   Moon I, Powers P, Shelton J, Shingara J;
XX
DR   WPI; 2006-047544/05.
XX
PT   Multi-labeling miRNA in a sample, by forming a reaction mixture for
PT   enzyme catalysis, where tailed miRNA molecules are produced, and
PT   attaching a label to the tailed miRNA molecules.
XX
PS   Disclosure; SEQ ID NO 215; 307pp; English.
```

The new invention relates to manipulation of miRNA and their use in
characterizing their role and function in cells. Described is a method of
multi-labeling miRNA in a sample by forming a reaction mixture for enzyme
catalysis, comprising the miRNA with an enzyme that catalyzes the
addition of di- or tri-phosphate nucleotide, and one or more labeled or
unlabeled nucleotides, where tailed miRNA molecules are produced; and
attaching a label to the tailed miRNA molecules. Specifically, the method
comprises enriching miRNA in the sample; forming a reaction mixture,
under conditions that allows for catalysis, where tailed miRNA
molecules are produced; and if unlabeled nucleotides are added to the
miRNA, attaching a label to the tailed miRNA molecules. Also given
include a miRNA array comprising one or more miRNA probes immobilized on
a solid support, where the probes comprise an miRNA coding sequence, and
an amine attached to the 5' or 3' end of the probe; evaluating miRNA expression and a disease
sample; identifying a correlation between miRNA expression and a disease

```
CC   or condition; analyzing miRNA in a sample; identifying a candidate
CC   diagnostic marker or therapeutic target of a disease or condition;
CC   determining a difference between two or more biological samples;
CC   screening for a candidate therapeutic agent for a disease or condition;
CC   and a kit for preparing miRNA for multi-labeling. The methods and
CC   compositions are useful for isolating, enriching, and/or labeling miRNA
CC   molecule samples. The present sequence is a mouse miRNA sequence, used in
CC   the new methods of the invention.
XX
SQ   Sequence 83 BP; 26 A; 15 C; 22 G; 0 T; 20 U; 0 Other;

Query Match             82.7%;  Score 68.6;  DB 15;  Length 83;
Best Local Similarity   94.7%;  Pred. No. 4.1e-15;
Matches 71;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAC 60

Qy  61 UGUGCUGCCUCAAAA 75
        |||||||||||||||
Db  61 UGUGCUGCCUCAAAA 75


RESULT 12
ADX04205
ID   ADX04205 standard; RNA; 70 BP.
XX
AC   ADX04205;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Mouse primary-microRNA (pri-miRNA) mir-15a.
XX
KW   MicroRNA; ds; RNA interference; gene silencing; Cytostatic; Antidiabetic;
KW   Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
KW   Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW   Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW   angiogenesis disorder; cardiovascular disease;
KW   non-insulin dependent diabetes; metabolic disorder; endocrine disease;
KW   gastrointestinal disease; metabolic disorder; obesity;
KW   nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
KW   hypertension; anorexia nervosa; nutritional disorder;
KW   psychiatric disorder; Alzheimers disease; degeneration;
KW   neurological disease; nervous system injury; neurodegenerative disease;
KW   neurological disorder.
XX
OS   Mus sp.
XX
PN   WO200513901-A2.
XX
PD   17-FEB-2005.
XX
PF   30-JUL-2004; 2004WO-US025300.
XX
PR   31-JUL-2003; 2003US-0492056P.
PR   31-OCT-2003; 2003US-0516303P.
PR   19-DEC-2003; 2003US-0531596P.
PR   14-APR-2004; 2004US-0562217P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BP;
PI   Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;
PI   Peralta E;
XX
DR   WPI; 2005-163123/17.
XX
PT   New oligomeric compound that can hybridize with or sterically interfere
PT   with nucleic acid molecules comprising or encoding small non-coding RNA
PT   targets, useful for treating e.g. cancer and diabetes.
XX
PS   Example 34; SEQ ID NO 1316; 854pp; English.
```

XX
CC The invention relates to an oligomeric compound comprising a first region
CC and a second region, where at least one region contains a modification,
CC and a portion of the oligomeric compound is targeted to a small non-
CC coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC comprising a first oligomeric compound and a second oligomeric compound
CC (where at least one of the oligomeric compounds is capable of
CC hybridizing with at least a portion of the second oligomeric compound,
CC and at least a portion of the first oligomeric compound is targeted to a
CC small non-coding RNA target nucleic acid), a pharmaceutical composition
CC comprising the composition cited above (and a carrier), a kit or assay
CC device comprising the composition, modulating the expression of a small
CC non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC treating or preventing a disease or disorder associated with a small non-
CC coding RNA target nucleic acid, treating a condition in an animal,
CC treating or preventing a disease or disorder associated with CD36,
CC methods of screening an oligomeric compound for an effect on miRNA
CC signaling, methods of screening a miRNA precursor for an effect in miRNA
CC signaling, methods of modulating translation (or apoptosis, conversion of
CC a precursor miRNA into mRNA, or cellular differentiation), identifying
CC an RNA transcript bound to a small non-coding RNA, arresting (or
CC delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC segregation, identifying a miRNA target, modulating cellular
CC precursor, identifying a miRNA target, modulating cellular
CC differentiation, treating a condition associated with adipocyte
CC differentiation, treating/preventing a disease/disorder
CC associated with aberrant regulation of the cell cycle by miRNAs,
CC maintaining a pluripotent stem cell and identifying a small non-coding
CC RNA binding site. The oligomeric compound is targeted to a region
CC flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC increase in expression of a pri-miRNA. The compounds and compositions are
CC useful for treating a disease or disorder resulting from chromosomal non-
CC disjunction, altered methylation, acetylation, or pseudouridylation state
CC of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC hyperlipidemia, atherosclerosis, hypertension, anorexia,
CC Alzheimer's disease, a central nervous system injury or neurodegenerative
CC disorder. The present sequence is a primary miRNA of the invention.
XX
SQ Sequence 70 BP; 23 A; 12 C; 18 G; 0 T; 17 U; 0 Other;

Query Match 74.5%; Score 61.8; DB 14; Length 70;
Best Local Similarity 96.9%; Pred. No. 1.2e-12;
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 AAGUAGCAGCACAUAAUGGUUUGUGGGGAUUUUGAAAAAGGUGCAGGCGCCAUAUUGUGCUGCCU 70
   ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 1 AAGUAGCAGCACAUAAUGGUUUGUGGGGAUUUGUGAAAAAGGUGCAGGCGCCAUACUGUGCUGCCU 60

Qy 71 CAAAA 75
   |||||
Db 61 CAAAA 65

RESULT 13
ID AEB92912 standard; DNA; 40 BP.
XX
AC AEB92912;
XX
DT 03-NOV-2005 (first entry)
XX
DE Human microRNA gene probe SEQ ID NO 325.
XX
KW cytostatic; gene therapy; diagnosis; prognosis; pharmaceutical;
KW gene expression; musculoskeletal disease; hematological disease;
KW immunostimulant; andrology; neurological disease; dermatological disease;
KW endocrine disease; gynecology and obstetrics; respiratory disease;
KW gastrointestinal disease; genitourinary disease; cancer; neoplasm;
KW microRNA; miR; ss; biochip; probe.

XX
OS Homo sapiens.
XX
PN WO200507139-A2.
XX
PD 25-AUG-2005.
XX
PF 09-FEB-2005; 2005WO-US004865.
XX
PR 09-FEB-2004; 2004US-0542929P.
PR 09-FEB-2004; 2004US-0542940P.
PR 09-FEB-2004; 2004US-0542963P.
PR 09-FEB-2004; 2004US-0543119P.
PR 18-JUN-2004; 2004US-0580797P.
PR 18-JUN-2004; 2004US-0580959P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Liu C, Calin GA;
XX
DR WPI; 2005-571622/58.
XX
PT Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,
PT tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in
PT the test sample.
XX
PS Example 10; SEQ ID NO 325; 170pp; English.
XX
CC The invention describes diagnosing whether a subject has, or is at risk
CC for developing, a cancer linked to a cancer-associated chromosomal
CC feature, comprises evaluating the status in the subject of at least one
CC microRNA (miR) gene located in close proximity to the cancer-associated
CC chromosomal feature. Also described are a pharmaceutical composition
CC comprising an isolated miR gene product or a nucleic acid encoding an
CC isolated miR gene product from an miR gene located in close proximity to
CC a cancer-associated chromosomal feature and is not miR15 or miR16, and a
CC pharmaceutical carrier; and a method of treating cancer associated with a
CC cancer-associated chromosomal feature in a subject. The miR, composition,
CC and method are useful for diagnosing and treating a cancer-associated
CC chromosomal feature, where the cancer is bladder cancer, esophageal
CC cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer
CC ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic
CC tumors, solid tumors, gastric cancer, colorectal cancer, hepatic cancer,
CC epithelial cancer, nasopharyngeal cancer, uterine cancer, malignant
CC head-and-neck cancer, renal cancer, male germ cell tumors,
CC melanoma, myelodysplastic syndrome, pancreatic or biliary cancer,
CC prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilm's
CC tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,
CC neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid
CC leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,
CC medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
CC chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
CC associated with an unmutated IgVH gene, ZAP-70 expression, CD38
CC expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
CC their combination. This sequence represents a human microRNA (miRNA) gene
CC probe used in the creation of an oligonucleotide microchip for miRNA
CC profiling.
XX
SQ Sequence 40 BP; 11 A; 5 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 48.2%; Score 40; DB 14; Length 40;
Best Local Similarity 67.5%; Pred. No. 0.00011;
Matches 27; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGGGAUUU 40
   ||:||||||||||:||||||||:||:||:||||:||||||:::
Db 1 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGGATTT 40

RESULT 14
ID AEB92913 standard; DNA; 40 BP.
XX
AC AEB92913;

```
XX
DT   03-NOV-2005 (first entry)
XX
DE   Human microRNA gene probe SEQ ID NO 326.
XX
KW   cytostatic; gene therapy; diagnosis; prognosis; pharmaceutical;
KW   gene expression; musculoskeletal disease; hematological disease;
KW   immunostimulant; andrology; neurological disease; dermatological disease;
KW   endocrine disease; gynecology and obstetrics; respiratory disease;
KW   gastrointestinal disease; genitourinary disease; cancer; neoplasm;
KW   microRNA; miR; ss; biochip; probe.
XX
OS   Homo sapiens.
XX
PN   WO2005078139-A2.
XX
PD   25-AUG-2005.
XX
PF   09-FEB-2005; 2005WO-US004865.
XX
PR   09-FEB-2004; 2004US-0542929P.
PR   09-FEB-2004; 2004US-0542940P.
PR   09-FEB-2004; 2004US-0542963P.
PR   09-FEB-2004; 2004US-0543119P.
PR   18-JUN-2004; 2004US-0580797P.
PR   18-JUN-2004; 2004US-0580959P.
XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Croce CM, Liu C, Calin GA;
XX
DR   WPI; 2005-571622/58.
XX
PT   Diagnosing a cancer-associated chromosomal feature, e.g. bladder cancer,
PT   tumors, or myelodysplastic syndrome, comprises evaluating a miR gene in
PT   the test sample.
XX
PS   Example 10; SEQ ID NO 326; 170pp; English.
XX
CC   The invention describes diagnosing whether a subject has, or is at risk
CC   for developing, a cancer linked to a cancer-associated chromosomal
CC   feature, comprises evaluating the status in the subject of at least one
CC   microRNA (miR) gene located in close proximity to the cancer-associated
CC   chromosomal feature. Also described are a pharmaceutical composition
CC   comprising an isolated miR gene product or a nucleic acid encoding an
CC   isolated miR gene product from an miR gene located in close proximity to
CC   a cancer-associated chromosomal feature and is not miR15 or miR16, and a
CC   pharmaceutical carrier; and a method of treating cancer associated with a
CC   cancer-associated chromosomal feature in a subject. The miR, composition,
CC   and method are useful for diagnosing and treating a cancer-associated
CC   chromosomal feature, where the cancer is bladder cancer, esophageal
CC   cancer, lung cancer, stomach cancer, kidney cancer, cervical cancer,
CC   ovarian cancer, breast cancer, lymphoma, Ewing sarcoma, hematopoietic
CC   tumors, solid tumors, gastric cancer, colorectal cancer, brain cancer,
CC   epithelial cancer, nasopharyngeal cancer, uterine cancer, hepatic cancer,
CC   head-and-neck cancer, renal cancer, male germ cell tumors, malignant
CC   mesothelioma, myelodysplastic syndrome, pancreatic or biliary cancer,
CC   prostate cancer, thyroid cancer, urothelial cancer, renal cancer, Wilm's
CC   tumor, small cell lung cancer, melanoma, skin cancer, osteosarcoma,
CC   neuroblastoma, leukemia (acute lymphocytic leukemia, acute myeloid
CC   leukemia, chronic lymphocytic leukemia), glioblastoma multiforme,
CC   medulloblastoma, lymphoplasmacytoid lymphoma, rhabdomyosarcoma, B-cell
CC   chronic lymphocytic leukemia, or B-cell chronic lymphocytic leukemia
CC   associated with an unmutated IgVH gene, ZAP-70 expression, CD38
CC   expression, a deletion at chromosome 11q23, a loss or mutation of TP53 or
CC   their combination. This sequence represents a human microRNA (miRNA) gene
CC   probe used in the creation of an oligonucleotide microchip for miRNA
CC   profiling.
XX
SQ   Sequence 40 BP; 8 A; 6 C; 12 G; 14 T; 0 U; 0 Other;

Query Match             48.2%;  Score 40;  DB 14;  Length 40;
Best Local Similarity   65.0%;  Pred. No. 0.00011;

Matches  26;  Conservative  14;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  30 UUUGUGGAUUUUGAAAAGGUGCAGGCCAUAUUGUGCUGCC 69
        :::|:|||:::||||||||||||||||||:|:|:||:|||
Db   1 TTTGTGGATTTTGAAAAGGTGCAGGCCATATTGTGCTGCC 40

RESULT 15
AD017089/c
ID   AD017089 standard; RNA; 83 BP.
XX
AC   AD017089;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human miR15 precursor RNA sequence SeqID1.
XX
KW   miR15; miR16; cancer; proliferation; cancer cell; cytostatic;
KW   gene therapy; chronic lymphocytic leukaemia; prostate cancer; micro RNA;
KW   chromosome 13q14; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1..5
FT                   /tag= a
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 83-79
FT                   of itself"
FT   misc_binding    16..23
FT                   /tag= b
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 68-61
FT                   of itself"
FT   misc_binding    26..35
FT                   /tag= c
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 58-49
FT                   of itself"
FT   misc_binding    38..40
FT                   /tag= d
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 46-44
FT                   of itself"
FT   misc_binding    44..46
FT                   /tag= e
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 40-38
FT                   of itself"
FT   misc_binding    49..58
FT                   /tag= f
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 35-26
FT                   of itself"
FT   misc_binding    61..68
FT                   /tag= g
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 23-16
FT                   of itself"
FT   misc_binding    79..83
FT                   /tag= h
FT                   /bound_moiety= "Binds to itself"
FT                   /note= "Forms a double stranded region with bases 5-1 of
FT                   itself"
XX
PN   WO2004043387-A2.
XX
PD   27-MAY-2004.
XX
PF   12-NOV-2003; 2003WO-US035777.
XX
PR   13-NOV-2002; 2002US-0425864P.
PR   09-MAY-2003; 2003US-0469464P.
```

XX
PA   (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI   Croce CM, Calin GA;
XX
DR   WPI; 2004-400825/37.
XX
XX
PT   Treating an miR15 or miR16 mediated cancer, i.e. chronic lymphocytic
PT   leukemia or prostate cancer, comprises administering to the subject an
PT   miR15 or miR16 gene product.
XX
PS   Claim 64; SEQ ID NO 1; 73pp; English.
XX
XX
CC   This invention relates to a novel method of treating an miR15 or miR16
CC   mediated cancer in a subject which comprises administering to the subject
CC   an amount of an isolated miR15 or miR16 gene product such that
CC   proliferation of miR15 or miR16 mediated cancer cells in inhibited. The
CC   miR15 and miR16 micro RNA genes are localised to 13q14 in humans, a
CC   region that is deleted in a significant portion of subjects suffering
CC   from chronic lymphocytic leukaemia or prostate cancer. The products of
CC   the miR15 and miR16 genes have also been found to inhibit the neoplastic
CC   or tumourigenic growth of chronic lymphocytic leukaemia or prostate
CC   cancer cells. The invention may be useful for the production of compounds
CC   with a cytostatic activity. In addition the invention may also be useful
CC   for gene therapy using the miR15 or miR16 gene product. The methods and
CC   compositions are useful in diagnosing and treating miR15 or miR16
CC   mediated cancer, i.e. chronic lymphocytic leukaemia or prostate cancer.
CC   The present sequence is that of the human miR15 precursor RNA sequence
CC   which is used in the method of the invention.
XX
SQ   Sequence 83 BP; 26 A; 13 C; 22 G; 0 T; 22 U; 0 Other;

Query Match   40.2%;   Score 33.4; DB 12; Length 83;
Best Local Similarity 45.8%;   Pred. No. 0.036;
Matches   38; Conservative 14; Mismatches 31; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
              ||:||:|| |: |||||||||| | |:|: | :| :::: |||| ||| |||||||
Db   83 CCTTGTATTTTTGAGGCAGCACAATATGGCCTGCACCTTTCAAAATCCACAAACCATTA 24

Qy   61 UGUGCUGCCUCAAAAAUACAAGG 83
              :|:||:||:|| | |:|||||||
Db   23 TGTGCTGCTACTTTACTCCAAGG 1

Search completed: November 1, 2006, 22:24:59
Job time : 399.61 secs

```
OM nucleic - nucleic search, using sw model

                    GenCore version 5.1.9
                    Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:             November 1, 2006, 20:21:19 ; Search time 3848.83 Seconds
                                                (without alignments)
                                                1205.901 Million cell updates/sec

Title:              US-10-706-798-1
Perfect score:      83
Sequence:           1 ccuggaguaaguagcagc..........gcugccucaaaauacaagg 83
Scoring table:      IDENTITY_NUC
                    Gapop 10.0, Gapext 1.0
Searched:           48236798 seqs, 2795966S780 residues
Total number of hits satisfying chosen parameters:              96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  EST:*
     1: gb_est1:*
     2: gb_est3:*
     3: gb_est4:*
     4: gb_est5:*
     5: gb_est6:*
     6: gb_htc:*
     7: gb_est2:*
     8: gb_est7:*
     9: gb_est8:*
    10: gb_est9:*
    11: gb_gss1:*
    12: gb_gss2:*
    13: gb_gss3:*
    14: gb_gss4:*
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	77.2	93.0	486	11	AQ672199	AQ672199 HS_2151_B
c 2	71.8	86.5	638	11	DA287889	DA287889 DA287889
c 3	44.3	44.3	330	14	AZ938498	AZ938498 2M0197A08
c 4	41.4	41.4	893	14	DR22A19S	DR22A19S Danio rer
c 5	39.0	41.4	486	11	CNS032XX	CNS032XX Tetraodon
c 6	37.3	32.4	348	10	AQ672199	AQ672199 HS_2151_B
c 7	36.9	31	690	8	DR975958	DR975958 Skin-13_B
c 8	36.9	30.6	409	8	AQ830728	CV259755 2M0110F10
c 9	36.6	30.4	669	11	CV259755	CV259755 WS02012.B
c 10	36.6	30.4	657	12	AZ955179	AZ955179 2M0221K10
c 11	36.1	30	901	14	CK791915	CK791915 AGENCOURT
c 12	36.1	30	657	12	CT224114	CT224114 Sus scrof
c 13	35.9	29.8	752	7	CX206707	CX206707 MNS11072
c 14	35.2	29.2	832	7	BE538951	BE538951 601061142
c 15	34.9	29	266	1	AL701112	AL701112 DKFZp686M
c 16	34.9	29	893	14	CB503344	CB503344 ssalmge50
c 17	34.7	28.8	557	7	BE228377	BE228377 98AS1771
c 18	34.7	28.8	797	9	CX492605	CX492605 JGI_XZG38
c 19	34.7	28.8	820	9	CX405012	CX405012 JGI_XZT36
c 20	34.7	28.8	822	11	BZ117274	BZ117274 CH230-411
c 21	34.5	28.6	541	9	DA287889	DA287889 DA287889
c 22	34.5	28.6	765	14	CT385120	CT385120 Sus scrof
c 23	34.5	28.6	793	12	CC925298	CC925298 t083b14ba
c 24	34.2	28.4	445	12	CE142086	CE142086 tigr-gss-
c 25	34.2	28.4	633	13	CW371850	CW371850 fabb001f0
c 26	34.2	28.4	786	9	CX829205	CX829205 JGI_CAAK6
c 27	34.2	28.4	1019	12	CL039913	CL039913 CH216-48M
c 28	34.0	28.2	538	8	CO159141	CO159141 FtD1_11_E
c 29	34.0	28.2	551	11	BZ148619	BZ148619 CH230-395
c 30	34.0	28.2	553	11	AQ693353	AQ693353 HS_5458_A
c 31	34.0	28.2	664	5	CF387823	CF387823 RTDR1_18_
c 32	34.0	28.2	691	8	CO366636	CO366636 RTK1_29_C
c 33	34.0	28.2	719	8	CF387852	CF387852 RTK1_29_C
c 34	34.0	28.2	829	11	BZ205743	BZ205743 EST957868
c 35	34.0	28.2	835	9	DN462069	DN462069 EST957868
c 36	34.0	28.2	906	13	CL992915	CL992915 ZMMBHf000
c 37	34.0	28.2	908	10	DT626902	DT626902 EST115997
c 38	34.0	28.2	917	13	CZ792260	CZ792260 OC_Ba015
c 39	33.7	28	433	5	CK058325	CK058325 58617rsic
c 40	33.7	28	446	1	AU173105	AU173105 AU173105
c 41	33.7	28	466	5	CK048847	CK048847 47887rsic
c 42	33.7	28	516	5	CK035528	CK035528 35211rsic
c 43	33.7	28	536	5	CK083202	CK083202 81007rsic
c 44	33.7	28	543	14	AL088951	AL088951 Arabidops
c 45	33.7	28	549	9	CX632947	CX632947 GBN003N23

```
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

RESULT 1

AQ672199/c

```
LOCUS       AQ672199      486 bp    DNA     linear   GSS 24-JUN-1999
DEFINITION  HS_2151_B1_B12_MR_CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2151 Col=23 Row=D, genomic survey
            sequence.
ACCESSION   AQ672199
VERSION     AQ672199.1  GI:5204870
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  PUBMED    10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3087
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 2151 row: D column: 23
            Seq primer: M13 Reverse
            Class: BAC ends
            High quality sequence stop: 486.
FEATURES             Location/Qualifiers
     source          1..486
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=2151 Col=23 Row=D"
                     /sex="male"
```

ALIGNMENTS

ORIGIN
          /clone_lib="CIT Approved Human Genomic Sperm Library D"
          /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
          E-Coli DH10B"

Query Match
Best Local Similarity   93.0%;   Score 77.2; DB 11; Length 486;
68.7%;   Pred. No. 3.1e-15;
Matches 57; Conservative 22; Mismatches 4; Indels 0; Gaps 0;

Qy   1 CCUUGGAGUAAAGUAGCCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
Db 440 CGUUGNAGUAAAGUAGCAGCACAUAANGGUUUNGUGAUUUGAAAAGGUGCAGGCCAUAU 381

Qy 61 UGUGCUGCCUCAAAAAUACAAGG 83
Db 380 TGTGCTGCCTCAAGAATACAAGG 358

RESULT 2
LOCUS   AZ938498/c   638 bp   DNA   linear   GSS 26-APR-2001
DEFINITION AZ938498 2M0197A08F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0197A08 F, genomic survey sequence.
ACCESSION   AZ938498
VERSION   AZ938498.1 GI:13798291
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 638)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0197   row: A   column: 08
            Seq primer: CGTTGTAAAACCACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 638.
FEATURES   Location/Qualifiers
     source   1..638
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0197A08"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Query Match
Best Local Similarity   86.5%;   Score 71.8; DB 11; Length 638;
72.0%;   Pred. No. 2.2e-13;
Matches 54; Conservative 19; Mismatches 2; Indels 0; Gaps 0;

Qy   1 CCUUGGAGUAAAGUAGCCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
Db 201 CCTTGGAGTAAAGTAGCAGCAGCACATAATGGTTTGTGGATGNTTGAAAAGGTGCAGGCCATAC 142

Qy 61 UGUGCUGCCUCAAAA 75
Db 141 TGTGCTGCCTCAAAA 127

RESULT 3
LOCUS   DR22A19S   330 bp   DNA   linear   GSS 27-NOV-2002
DEFINITION DR22A19S Danio rerio genomic clone DKEY-22A19, genomic survey sequence.
ACCESSION   AL739377
VERSION   AL739377.1 GI:21348782
KEYWORDS   GSS.
SOURCE   Danio rerio (zebrafish)
  ORGANISM Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 330)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE   Direct Submission
  JOURNAL   Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgehire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT   This sequence was generated from the SP6 end of BAC 22A19, 22A19 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES   Location/Qualifiers
     source   1..330
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-22A19"
                     /clone_lib="DKEY-22A19"
                     /tissue_type="Testis"
                     /note="vector pindigoBAC-536"
ORIGIN

Query Match
Best Local Similarity   44.3%;   Score 36.8; DB 14; Length 330;
52.4%;   Pred. No. 0.17;
Matches 44; Conservative 17; Mismatches 22; Indels 1; Gaps 1;

Qy   1 CCUUGGAGUAAAGUAGGCAGCACAUAAUGGUUUGUGGAUUUUGA-AAAGGUGCAGGCCAUA 59
Db 149 CCTGTCGGTACTGTAGCAGCACATAATGGTTTGTGAGTATAACGGGGGGTGCAGGCCGTA 208

Qy 60 UUGUGCUGCCUCAAAAAUACAAGG 83
Db 209 CTGTGCTGCGCCAACACGACAGG 232

RESULT 4
LOCUS   CNS032XX   893 bp   DNA   linear   GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
            207L24 of library G from Tetraodon nigroviridis, genomic survey

```
            sequence.
ACCESSION   AL225438
VERSION     AL225438.1   GI:7884333
KEYWORDS    GSS; Genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 893)
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
   PUBMED   10835645
REFERENCE   2 (bases 1 to 893)
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
   PUBMED   10899143
REFERENCE   3 (bases 1 to 893)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1..893
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="207L24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG207DF12LP1
                     end : T"
ORIGIN
```

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Qy          13 GUAGCAGCACGAUAAUGGGUGUGGAUUUUGAAAAAGGUGCAGGCCAUAUUUGUGCUCCCCA 72
               ||:|||||||||  |||:|||:||:|  :||    |||||||||:| ||| :|||| ||||||
Db         630 GUAGCAGCACGGAAUCGGUUUCGUGAGUUACACUGAGAUUACAAGCCAUGCUGUGCCGGCA 689
```

```
RESULT 5
Query Match    41.4%;  Score 34.4;  DB 14;  Length 893;
Best Local Similarity   51.7%;  Pred. No. 1.3;
Matches   31;  Conservative  13;  Mismatches  16;  Indels  0;  Gaps  0;
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```
LOCUS       AQ672199    486 bp   DNA   linear   GSS 24-JUN-1999
DEFINITION  HS_2151_B1_B12_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2151 Col=23 Row=D, genomic survey
            sequence.
ACCESSION   AQ672199
VERSION     AQ672199.1   GI:5204870
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 486)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
```

```
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            sequencing the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel.: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 2151  row: D  column: 23
            Seq primer: M13 Reverse
            Class: BAC ends
            High quality sequence stop: 486.
FEATURES             Location/Qualifiers
     source          1..486
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="plate=2151 Col=23 Row=D"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN
```

```
Qy           1 CCUUGGAGUAAAGUAGCAGCGACACAUAAUGGGUGUGGAUUUUGAAAAAGGUGCAGGCCAU 60
               |||:||| |  | ||||||||   |||||||||||||||||||||||||| |||||||||
Db         358 CCUUGUAUUCUUGAGGCGAGGCACACAAUAUGGCCUGCUGCACCUUUCAAAAUACACAAAC 417

Qy          61 UGUGCUCGCCUCAAAAAAUACAAGG 83
               |:|||:| | ||||||||| |||||
Db         418 TGTGCTGCTACTTACTNCAACG 440
```

```
RESULT 6
Query Match    39.0%;  Score 32.4;  DB 11;  Length 486;
Best Local Similarity   44.6%;  Pred. No. 5.7;
Matches   37;  Conservative  14;  Mismatches  32;  Indels  0;  Gaps  0;
```

```
LOCUS       DR975958/c          348 bp   mRNA  linear  EST 03-JAN-2006
DEFINITION  Skin-13_B03_pDNR-LIB-SFI1A A. transmontanus skin express library
            Acipenser transmontanus cDNA, mRNA sequence.
ACCESSION   DR975958
VERSION     DR975958.1   GI:84178869
KEYWORDS    EST.
SOURCE      Acipenser transmontanus (white sturgeon)
  ORGANISM  Acipenser transmontanus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
            Acipenser.
REFERENCE   1 (bases 1 to 348)
  AUTHORS   Mariani,V., Malinverni,R. and Giuffra,E.
  TITLE     Transcriptome analysis of the American sturgeon (Acipenser
            transmontanus): pathways of gene expression in the spleen and skin
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Valentina Mariani
            Livestock Genomics 1
            PTP-CERSA
            Via Einstein, Loc. Ca.na Codazza, 26900 Lodi (LO), Italy
            Email: valentina.mariani@tecnoparco.org.
FEATURES             Location/Qualifiers
     source          1..348
                     /organism="Acipenser transmontanus"
                     /mol_type="mRNA"
                     /db_xref="taxon:7904"
                     /clone_lib="A. transmontanus skin express library"
                     /note="Organ: skin"
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RESULT 7
AZ830728

```
ORIGIN
Query Match        37.3%;   Score 31;   DB 10;   Length 348;
Best Local Similarity   47.1%;   Pred. No. 16;
Matches 40;   Conservative 18;   Mismatches 25;   Indels 2;   Gaps 1;

Qy    1 CCUUGGAGUAAAGUAGCAGCACAUAUGGUUUG--UGGAUUUUGAAUAAAGGUGGCAGGCCAU 58
          ||::| |||||| ||| ||:||| ::|:||||| :|:||||:||:||||
Db  242 CCUUAAAGUACUGUUAGGCAGCACAUCAUGGUUUGCAACACUAUAGUAGUUAAAGAUGCGAACCAT 183

Qy   59 AUUGUGCUGCCUCAAAAAUACAAGG 83
          :||:||:||| ||||||||||
Db  182 TAUUCGCUGCUUUAGAAUUUUAAGG 158
```

LOCUS   AZ830728   690 bp   DNA   linear   GSS 20-FEB-2001
DEFINITION   2M01l0F10F Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGC2M01l0F10 F, genomic survey sequence.
ACCESSION   AZ830728
VERSION   AZ830728.1 GI:13000636
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 690)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE   Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
             University of Utah
             University of Utah Genome Center
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000   Std Error: 0.00
             Plate: 0110   row: F   column: 10
             Seq primer: CGTTGTAAAACGACGGCCAGT
             Class: plasmid ends
             High quality sequence stop: 690.
FEATURES   Location/Qualifiers
     source 1..690
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /clone="UUGC2M01l0F10"
             /sex="Male"
             /clone_lib="Mouse 10kb plasmid UUGClM library"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1|), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

RESULT 8
CV259755/c

```
ORIGIN
Query Match        36.9%;   Score 30.6;   DB 11;   Length 690;
Best Local Similarity   46.8%;   Pred. No. 25;
Matches 36;   Conservative 12;   Mismatches 29;   Indels 0;   Gaps 0;

Qy    7 AGUAAAGUAGCAGCACAUAUGGUUUGUGGAUUUUGAAUAAAGGUGGCAGGCCAUAUUGUGCU 66
          |:| ||||| ||||||| ||||| :|||||| ::||||||||:||||| :|||||||||| :|
Db  213 AGATATGTGGCAGGTCATAACTTCTTCCTTTATCTGGCAAAAGCTCCGTGCCGCCATTTGCTGTC 272

Qy   67 GCCUCAAAAAUACAAGG 83
          ||:|||||| ||||
Db  273 ACCTCAAAAAAGAGAAAG 289
```

LOCUS   CV259755   409 bp   mRNA   linear   EST 22-SEP-2004
DEFINITION   WS02012_B21_D02 PTxN-IB-N-A-11 Populus trichocarpa x Populus nigra cDNA clone WS02012_D02 3', mRNA sequence.
ACCESSION   CV259755
VERSION   CV259755.1 GI:52512730
KEYWORDS   EST.
SOURCE   Populus trichocarpa x Populus nigra
ORGANISM   Populus trichocarpa x Populus nigra
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE   1 (bases 1 to 409)
AUTHORS   Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y., Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and Bohlmann,J.
TITLE   The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
JOURNAL   Unpublished (2004)
COMMENT   Contact: Joerg Bohlmann
             Genome BC forest genomics program
             University of British Columbia
             Michael Smith Laboratories, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 1Z3
             Tel: 1-604-822-0282
             Fax: 1-604-822-2114
             Email: bohlmann@msl.ubc.ca
             Plate: WS02012   row: D   column: 02
             High quality sequence stop: 409
             POLYA=Yes.
FEATURES   Location/Qualifiers
     source 1..409
             /organism="Populus trichocarpa x Populus nigra"
             /mol_type="mRNA"
             /cultivar="NxM6"
             /db_xref="taxon:293756"
             /clone="WS02012_D02"
             /sex="Male"
             /lab_host="E. coli DH10B T1 phage resistant cells"
             /clone_lib="PTxN-IB-N-A-11"
             /note="Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees two metres in height and grown under greenhouse conditions were exposed to continuous feeding by Cryptorhynchus lapathi (poplar and willow borer) adults caged on the sapling using mesh bags. Bark (with phloem and cambium attached) from within the caged region was harvested 2 hours, 6 hours and 48 hours after the onset of treatment. mRNA was isolated from each tissue source independently

RESULT 9

ORIGIN and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

```
Query Match      36.6%;  Score 30.4;  DB 8;  Length 409;
Best Local Similarity  42.5%;  Pred. No. 27;
Matches  34;  Conservative 15;  Mismatches  31;  Indels  0;  Gaps  0;

Qy   2 CUUGGAGUAAAGUAGCAGCACAUAAAUGGUUUGUGGAUUUUGAAAAGGUUGCAGCGCCAUAUU 61
         || |||   ||||||| |||||     |||| ||| ||||||||| ||||| || ||  |||
Db  88 CTACAAGAAAAAGGAGAATTTTATTTGATTTGATTACTTATTATATAGATCTTGGCCCTCTT 29

Qy  62 GUGCUGCCUCAAAAAUACAA 81
         |:|:| |||||||||| ||
Db  28 GTGGTGAAUCAAAAAAAAAA 9
```

RESULT 9

LOCUS   AZ955179   669 bp   DNA   linear   GSS 27-APR-2001
DEFINITION   2M0221K10F Mouse 10kb plasmid UUGC2M0221K10 F, genomic survey sequence.
ACCESSION   AZ955179
VERSION   AZ955179.1 GI:13826406
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 669)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
             Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
             Niederhausern,A. and Wright,D., Weiss,R.
TITLE   Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000   Std Error: 0.00
             Plate: 0221 row: K column: 10
             Seq primer: CGTGTAAAACGACGGCCAGT
             Class: plasmid ends
             High quality sequence stop: 669.
FEATURES   Location/Qualifiers
source   1..669
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC2M0221K10"
             /sex="Female"
             /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC2M library"
             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

---

RESULT 10

ORIGIN (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      36.6%;  Score 30.4;  DB 11;  Length 669;
Best Local Similarity  43.8%;  Pred. No. 29;
Matches  28;  Conservative 15;  Mismatches  21;  Indels  0;  Gaps  0;

Qy  11 AAGUAGCAGCACAUAAAUGGUGUGUGGAUUUUGUGAAAAGGUUGCAGCGCCAUAUUGUGCUGCCU 70
        |||  || | ||||| |   |||  | ||||| |||  ||| | ||||| ||  |: |: |:||
Db 562 AAGAAGCTGAACATATTAGTTTAGGTTTTTAAAATAAGTATATATGCAATATATTTTCCCTTT 621

Qy  71 CAAA 74
        ||||
Db 622 CAAA 625
```

RESULT 10

LOCUS   CK791915   826 bp   mRNA   linear   EST 25-FEB-2004
DEFINITION   AGENCOURT 18660624 NIH_MGC_230 Mus musculus cDNA clone IMAGE:30846441 5', mRNA sequence.
ACCESSION   CK791915
VERSION   CK791915.1 GI:42803911
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 826)
AUTHORS   NIH-MGC http://mgc.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Shioko Kimura/Atsushi Yamada, (NCI, CCR)
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Plate: NDAM1149 row: i column: 10
             High quality sequence stop: 643.
FEATURES   Location/Qualifiers
source   1..826
             /organism="Mus musculus"
             /mol_type="mRNA"
             /db_xref="taxon:10090"
             /clones="IMAGE:30846441"
             /tissue_type="Pooled thyroids from 5 mice"
             /lab_host="DH10B TonA"
             /clone_lib="NIH_MGC_230"
             /note="Organ: thyroid; Vector: pExpress-1; Site_1: NotI; Site_2: NotI; RNA obtained from 5 normal wild-type mice

ORIGIN
           thyroid. cDNA was primed using oligo-dT primer:
           5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
           the EcoRV/NotI sites of pExpress-1. Size-selection 1.4 kb
           resulted in an average insert size of 1.2 kb. Normalized
           version of this library is NIH_MGC 189library constructed
           by Express Genomics (Frederick, MD). Note: this is a
           NIH_MGC Library."

Qy   7 AGUAAAGUAGCAGCACAUAAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCGCCAUAUUGUGCU 66
           ||:|| :||||||::||| ||||:||||||:|||||||||||||||||||||:|: |:
Db   570 AATATATTAACATGATTGAANTGGTGAAAAGGACTTTGAAAAGGTGAGGGCTTAACTTTGAT 629

Qy   67 GCCUCAAAAAUA 78
           ||:|| ||||:|
Db   630 CCTtGCATAAATA 641

RESULT 11
LOCUS   CE734321   657 bp   DNA   linear   GSS 30-SEP-2003
DEFINITION tigr-gss-dog-17000330179737 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION   CE734321
VERSION   CE734321.1 GI:37074441
KEYWORDS   GSS.
SOURCE   Canis familiaris (dog)
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1 (bases 1 to 657)
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
TITLE   The dog genome: survey sequencing and comparative analysis
JOURNAL   Science 301 (5641), 1898-1903 (2003)
PUBMED   14512627
COMMENT   Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirkness@tigr.org
            Class: shotgun.
FEATURES   Location/Qualifiers
     source   1..657
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /strain="Standard Poodle"
                     /db_xref="taxon:9615"
                     /clone_lib="Dog Library"
                     /note="Site_1: BstXI; Libraries were prepared from
                     peripheral blood"
ORIGIN

Query Match   36.1%; Score 30; DB 12; Length 657;
Best Local Similarity   42.9%; Pred. No. 40;
Matches   30; Conservative   15; Mismatches 25; Indels 0; Gaps 0;

Qy   12 AGUAGCAGCACAUAAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCGCCAUAUUGUGCUGCCUC 71
           ||:| | ||||||| || |||| |:: ||:| || :||||:| |:|| ||| ||||||
Db   564 AGTAAGAGCAAATCTTGCTGCTTGACTTGAACAGGAGCTGCAGGAGGAGCGACTGACTTTTTTGCTGCCTT 505

Qy   72 AAAAAUACAA 81
           |:|| ||||
Db   504 CAGACTAGAA 495

RESULT 12
LOCUS   CT224114   901 bp   DNA   linear   GSS 02-NOV-2005
DEFINITION Sus scrofa genomic clone CH242-234B11, genomic survey sequence.
ACCESSION   CT224114
VERSION   CT224114.1 GI:79766278
KEYWORDS   GSS.
SOURCE   Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 901)
AUTHORS   Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE   Direct Submission
JOURNAL   Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT   This sequence was generated from the SP6 end of BAC 234B11. 234B11
            is part of the CHORI-242 BAC Library created by P. de Jong. Further
            details: http://www.sanger.ac.uk/Projects/S_scrofa/.
FEATURES   Location/Qualifiers
     source   1..901
                     /organism="Sus scrofa"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9823"
                     /clone="CH242-234B11"
                     /tissue_type="White blood cells"
                     /note="vector pTARBAC1.3_BamHI
                     sex female"
ORIGIN

Query Match   36.1%; Score 30; DB 14; Length 901;
Best Local Similarity   48.6%; Pred. No. 42;
Matches   34; Conservative   11; Mismatches 25; Indels 0; Gaps 0;

Qy   11 AAGUAGCAGCACAUAAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCGCCAUAUUGUGCU 70
           || ||||||| |||| ||||| || ||:|| | |:|:| |||| |:|| ::|:
Db   480 AACTAACAGCATAAAAAGGGTTGTGGAAGATCTTATTAGTCCAGCAAAAAATTATTAAGACT 421

Qy   71 CAAAACAUACA 80
           |||| ||||
Db   420 CAAAACATACA 411

RESULT 13
LOCUS   CX206707   752 bp   mRNA   linear   EST 29-DEC-2004
DEFINITION MNS11072 Mouse Neurosphere Normalized cDNA library Mus musculus
            cDNA 5', mRNA sequence.
ACCESSION   CX206707
VERSION   CX206707.1 GI:56861999
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 752)
AUTHORS   Williams,C., Wirta,V., Lundeberg,J. and Frisen,J.
TITLE   Expressed sequence tags of cDNA clones from murine neurospheres
JOURNAL   Unpublished (2005)
COMMENT   Contact: Williams, C.
            Molecular Biotechnology
            Institution of Biotechnology
            AlbaNova University Center, KTH-Royal Institute of Technology,
            91 Stockholm, Sweden
            Tel: +468553783332.
            Fax: +4685537848.1
            Email: cecilia.williams@biotech.kth.se
            Seq primer: M13REW.
FEATURES   Location/Qualifiers

ORIGIN

source   1..752
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="MALE"
/tissue_type="Lateral wall of lateral ventricle"
/cell_type="Early passage neurosphere"
/dev_stage="Adult"
/clone_lib="Mouse Neurosphere Normalized cDNA library"
/note="Organ: Adult brain; Vector: pCMVsport6.0; A cDNA
library was constructed in pCMVsport6.0 from RNA isolated
from neurospheres of adult male and female mice. Custom
normalized cDNA library by Invitrogen/ResGen"

Qy   Query Match   35.9%;   Score 29.8;   DB 8;   Length 752;
Best Local Similarity   43.8%;   Pred. No. 47;
Matches   32;   Conservative   14;   Mismatches   27;   Indels   0;   Gaps   0;

Qy   11   AAGUAGCAGCACAUAAUGGUUUGUGGGAUUUGAGAAAAGGUGCAGGCCACUAUUGUGUGCUGCCU 70
            ||:| ::| |||:| ||| :| |||:| |||| || ||:|||| :
Db   429   AATGTGCTGTTACTTCCGATTTACCAGATTTTGGGGAGGTTGCTGCCCCATTCTGTGTCTT 488

Qy   71   CAAAAAUACAAGG 83
        |||||| :|||||
Db   489   CTCAAGTACAAGG 501

RESULT 14

LOCUS   BE538951
DEFINITION   601061142P1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447515 5',
mRNA sequence.
ACCESSION   BE538951
VERSION   BE538951.1   GI:9767596
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1   (bases 1 to 832)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8421 row: d column: 12
High quality sequence start: 4
High quality sequence stop: 563.
FEATURES   Location/Qualifiers
source   1..832
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3447515"
/cell_line="MGC36"
/lab_host="DH10B"
/clone_lib="NIH_MGC_10"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb library prepared by Life
Technologies."

ORIGIN

Query Match   35.2%;   Score 29.2;   DB 7;   Length 832;
Best Local Similarity   50.0%;   Pred. No. 77;
Matches   41;   Conservative   8;   Mismatches   33;   Indels   0;   Gaps   0;

Qy   2   CUUGGAGUAAGUAGCAGCACAUAAUGGUUUGUGUGGGAUUUGAGAAAAGGUGCAGGCCAUAUU 61
     |:| |||||| |||| || |:|||| |||:|||||| :||||:|: ||||| ::
Db   94   CTTACAGTAAAGTACCAACCAAAAAGTGGGGGGGGGTGGGAGGACAAAAAGGCAAAAGGCCCGTT 153

Qy   62   GUGCUGCCUCUAAAAAAUACAAGG 83
      ||||||| :||||||||||||
Db   154   TCTGAGCATCAAAAGGACCAGG 175

RESULT 15

LOCUS   AL701112
DEFINITION   DKFZp686M10120_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686M10120 5', mRNA sequence.
ACCESSION   AL701112
VERSION   AL701112.1   GI:19621645
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1   (bases 1 to 266)
AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Weil,B. and
Wiemann,S.
TITLE   EST (Ottenwaelder,B., Obermaier,B., Mewes,H.W., Weil,B. and
Wiemann,S.)
JOURNAL   Unpublished (2001)
COMMENT   Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert.
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
This clone (DKFZp686M10120) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
source   1..266
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686M10120"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match   34.9%;   Score 29;   DB 1;   Length 266;
Best Local Similarity   44.3%;   Pred. No. 74;
Matches   27;   Conservative   14;   Mismatches   20;   Indels   0;   Gaps   0;

Qy   20   CACAUAAUGGUUUGUGUGGGAUUUGAGAAAAGGUGCAGGCCAUAUUGUGUGCCUCAAAAAAUAC 79
      ||||| ||: :|||| |||:|:|:|| ||||| |||: |||||||: :|||||||
Db   164   CACATACATGTGATTAACACATTTTTCAAAATGTGCAGTCCACATGTTGTGGTTCATAAAAATACAA 105

Qy   80   A 80
      |
Db   104   A 104

Search completed: November 1, 2006, 22:21:04
Job time : 3851.83 secs

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: November 1, 2006, 20:59:58 ; Search time 143.867 Seconds
(without alignments)
1079.486 Million cell updates/sec

Title:
Perfect score: 83
Sequence: 1 ccuggaguaaaguaguagcagc...........gcugcucaaaauacaagg 83

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	34.9	33392	3	US-09-949-016-15172	Sequence 15172, A
2	27.6	33.3	4745	3	US-09-713-273A-19	Sequence 19, Appl
3	27.4	33.0	86439	3	US-09-949-016-11945	Sequence 11945, A
4	27.4	33.0	86440	3	US-09-949-016-16990	Sequence 16990, A
5	27.4	33.0	194915	3	US-09-949-016-15584	Sequence 15584, A
6	27	32.5	3396	3	US-09-949-016-16961	Sequence 16961,
7	27	32.5	3396	3	US-09-487-558B-71	Sequence 71, Appl
8	26.8	32.3	13614	3	US-09-614-221A-280	Sequence 280, App
9 c	26.8	32.3	745	4	US-09-949-002-814	Sequence 814, App
10 c	26.4	31.8	745	4	US-09-297-648-3922	Sequence 3922, Ap
11 c	26.4	31.8	1555	3	US-08-669-408B-9	Sequence 9, Appl
12 c	26	31.3	198942	3	US-09-949-016-13209	Sequence 13209, A
13 c	25.8	31.1	601	3	US-09-949-016-50534	Sequence 50534, A
14	25.8	31.1	1664976	3	US-08-916-421B-1	Sequence 1, Appli
15	25.8	31.1	1664976	3	US-09-692-570-1	Sequence 1, Appli
16	25.6	30.8	601	3	US-09-949-016-30704	Sequence 30704, A
17	25.6	30.8	601	3	US-09-949-016-30705	Sequence 30705, A
18	25.6	30.8	601	3	US-09-949-016-182111	Sequence 182111,
19	25.6	30.8	601	3	US-09-949-016-182112	Sequence 182112,
20	25.6	30.8	31602	3	US-09-949-016-16961	Sequence 16961,
21	25.6	30.8	36643	3	US-09-949-016-11860	Sequence 11860, A
22	25.6	30.8	36821	3	US-09-949-016-11403	Sequence 11403, A
23	25.6	30.8	139150	3	US-09-949-016-17398	Sequence 17398, A
24 c	25.6	30.8	139577	3	US-09-949-016-12879	Sequence 12879, A
25	25.4	30.6	6350	3	US-09-647-826-1	Sequence 1, Appli
26	25.4	30.6	162450	3	US-09-345-882-1	Sequence 1, Appli
27	25.4	30.6	162450	3	US-10-071-179-1	Sequence 1, Appli
28 c	25.2	30.4	601	3	US-09-949-016-169536	Sequence 169536,
29	25.2	30.4	601	3	US-09-949-016-169537	Sequence 169537,
30	25.2	30.4	160759	3	US-09-949-016-16514	Sequence 16514, A
31	25.2	30.4	197131	3	US-09-949-016-12675	Sequence 12675, A
32	25.2	30.4	197132	3	US-09-949-016-17170	Sequence 17170, A
33 c	25.2	30.1	198	3	US-09-248-796A-13614	Sequence 13614, A
34	25	30.1	601	3	US-09-949-016-126639	Sequence 126639,
35	25	30.1	601	3	US-09-949-002-2166	Sequence 2166, Ap
36	25	30.1	3004	3	US-09-949-002-10608	Sequence 10608, A
37	25	30.1	3110	3	US-09-023-655-1114	Sequence 1114, Ap
38	25	30.1	3110	3	US-09-949-002-277	Sequence 277, App
39	25	30.1	3415	2	US-08-054-077C-1	Sequence 52, Appli
40 c	25	30.1	7350	3	US-09-949-016-3602	Sequence 3602, Ap
41	25	30.1	86980	3	US-09-949-016-15344	Sequence 15344, A
42	25	30.1	114183	3	US-09-949-002-849	Sequence 849, App
43	25	30.1	127546	3	US-09-949-002-624	Sequence 624, App
44 c	25	30.1	254366	3	US-09-822-871-3	Sequence 3, Appli
45	25					

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-949-016-15172
; Sequence 15172, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15172
; LENGTH: 33392
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(33392)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-15172

Query Match 34.9%; Score 29; DB 3; Length 33392;
Best Local Similarity 37.7%; Pred. No 1.9;
Matches 29; Conservative 18; Mismatches 30; Indels 0; Gaps 0;

```
Qy      1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
            ||||| |||.||||.||||.||||||||  ||||.|.|:::.|.|:::|||:|||:||  |:|
Db  29986 CCAUAAGUUAAAUAAGUAAUAUAUAUAUUCUUUGUAAUUUCGUGAAGAGCUUUAGUUUAUAA 30045

Qy     61 UGUGCUGCCUCAAAAUU 77
            |:|:|.||:||:|| |:|
Db  30046 TGTTCUUUCCCCAUAUAU 30062
```

RESULT 2
US-09-713-273A-19
; Sequence 19, Application US/09713273A
; Patent No. 6620987

GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; TITLE OF INVENTION: STARCH R1 PHOSPHORYLATION PROTEINS
; FILE REFERENCE: BB1158 US CIP
; CURRENT APPLICATION NUMBER: US/09/713,273A
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/081,143
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: PCT/US99/07639
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 09/679,933
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Microsoft Office 97
;
; SEQ ID NO 19
; LENGTH: 4745
; TYPE: DNA
; ORGANISM: Glycine max
US-09-713-273A-19

Qy   Matches 34; Conservative 11; Mismatches 29; Indels 0; Gaps 0;
Db   Best Local Similarity 45.9%; Pred. No. 3.1;
        Query Match 33.3%; Score 27.6; DB 3; Length 4745;

Qy   3 UUGGAGUAAGUAGCAGCCACAUAAUGGUUUGUGGAUUUGUGAAAAGGUGCAGGCCAUAUG 62
          :::
Db   1706 UUGGUGGGAGGAAGCAGAAAACAGAGAGGAUUUUGGCAAUAUGGCAAAGGUACAGCCAAGUUCU 1765

Qy   63 UGCUGCCUCAAAAA 76
          :::::::::::::::
Db   1766 TGTTGAATAAAATA 1779

RESULT 3
US-09-949-016-11945
; Sequence 11945, Application US/0994901G
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 11945
; LENGTH: 86439
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11945

Qy   Matches 30; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
Db   Best Local Similarity 43.5%; Pred. No. 11;
        Query Match 33.0%; Score 27.4; DB 3; Length 86439;

Qy   9 UAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGUGAAAAGGUGCAGGCCAUAUUGUGCCUGC 68
          :::
Db 49398 TACACGAGATGCTGAAACTGTAATCTGGGTTCTGAACATGGGCCATTCCATGTGGTTCTCA 49457

Qy   69 CUCAAAAAU 77
          ::|||||||
Db 49458 TTCAAAATT 49466

RESULT 4

US-09-949-016-16990
; Sequence 16990, Application US/0994901G
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 16990
; LENGTH: 86440
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16990

Qy   Matches 30; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
Db   Best Local Similarity 43.5%; Pred. No. 11;
        Query Match 33.0%; Score 27.4; DB 3; Length 86440;

Qy   9 UAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGUGAAAAGGUGCAGGCCAUAUUGUGCCUGC 68
          :::
Db 49398 TACACGAGATGCTGAAACTGTAATCTGGGTTCTGAACATGGGCCATTCCATGTGGTTCTCA 49457

Qy   69 CUCAAAAAU 77
          ::|||||||
Db 49458 TTCAAAATT 49466

RESULT 5
US-09-949-016-15584
; Sequence 15584, Application US/0994901G
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 15584
; LENGTH: 194915
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(194915)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15584

Qy   Matches 32; Conservative 14; Mismatches 31; Indels 0; Gaps 0;
Db   Best Local Similarity 41.6%; Pred. No. 15;
        Query Match 33.0%; Score 27.4; DB 3; Length 194915;

Qy   3 UUGGAGUAAGUAGCAGCCACAUAAUGGUUUGUGGAUUUUGUGAAAAGGUGCAGGCCAUAUUG 62
          ::|||||||::::||||||::|::::::::::::||||||::::|||||::::||::::|||
Db   5285 TTAGATAAAAGATATAAGCAATAAAAATAATTATTGTTACTATTTGCAGGAGCAAAACTCTTTG 5344

```
Qy    63 UGCUGCCUCAAAAAUAC 79
         |||:||||:||||:||:|
Db  5345 AGCTGCCTCAACTATCC 5361
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RESULT 6
US-09-614-221A-280
Sequence 280, Application US/09614221A
Patent No. 6723837
GENERAL INFORMATION:
APPLICANT: Yu, Jaehyuk
APPLICANT: Kishore, Ganesh M.
APPLICANT: Karunanandaa, Balasulojini
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
FILE REFERENCE: 16516.075
CURRENT APPLICATION NUMBER: US/09/614,221A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/142,981
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 626
SEQ ID NO 280
LENGTH: 3396
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-280

Query Match   32.5%;   Score 27;   DB 3;   Length 3396;
Best Local Similarity   40.3%;   Pred. No. 4.6;
Matches 27;   Conservative 15;   Mismatches 25;   Indels 0;   Gaps 0;

```
Qy    13 GUAGCAGCACAUAAUGGUUUGUGGAUUUGUGAAAAAGGUGCAGGCCAUAUUGUGCUGCCUCA 72
Db  2173 GTCACAAAAAAAAAAAAAAAAATTGTAATTGGATTTTGAAATACTGCAGAGAAGTTCTTATGCTTCAACA 2232

Qy    73 AAAAUAC 79
Db  2233 GATGTAC 2239
```

Query Match   32.5%;   Score 27;   DB 3;   Length 3396;
Best Local Similarity   40.3%;   Pred. No. 4.6;
Matches 27;   Conservative 15;   Mismatches 25;   Indels 0;   Gaps 0;

```
Qy    13 GUAGCAGCACAUAAUGGUUUGUGGAUUUGUGAAAAAGGUGCAGGCCAUAUUGUGCUGCCUCA 72
Db  2173 GTCACAAAAAAAAAAAAAAAAATTGTAATTGGATTTTGAAATACTGCAGAGAAGTTCTTATGCTTCAACA 2232

Qy    73 AAAAUAC 79
Db  2233 GATGTAC 2239
```

RESULT 7
US-09-487-558B-71
Sequence 71, Application US/09487558B
Patent No. 6949356
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: Newman, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 71
LENGTH: 3396
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-71

Query Match   32.5%;   Score 27;   DB 3;   Length 3396;
Best Local Similarity   40.3%;   Pred. No. 4.6;
Matches 27;   Conservative 15;   Mismatches 25;   Indels 0;   Gaps 0;

```
Qy    13 GUAGCAGCACAUAAUGGUUUGUGGAUUUGUGAAAAAGGUGCAGGCCAUAUUGUGCUGCCUCA 72
Db  2173 GTCACAAAAAAAAAAAAAAAAATTGTAATTGGATTTTGAAATACTGCAGAGAAGTTCTTATGCTTCAACA 2232

Qy    73 AAAAUAC 79
Db  2233 GATGTAC 2239
```

RESULT 8
US-09-949-002-814
Sequence 814, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 814
LENGTH: 13614
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(13614)
OTHER INFORMATION: n = A,T,C or G
US-09-949-002-814

Query Match   32.3%;   Score 27;   DB 3;   Length 13614;
Best Local Similarity   44.3%;   Pred. No. 9.1;
Matches 31;   Conservative 12;   Mismatches 27;   Indels 0;   Gaps 0;

```
Qy     2 CUUGGAGUAAGAGUAGCAGCACAUAAUGGUUUGUGGAUUUGUGAAAAAGGUGCAGGCCAUAUU 61
Db  3261 CTTGCAGAACTGGATTAGTAATTAATAGAATGGGTATTATAGAGAGGGGTGCCCCTTTGT 3320

Qy    62 GUGCUGCCUC 71
Db  3321 GTTTTGCCCC 3330
```

RESULT 9
US-09-297-648-3922
Sequence 3922, Application US/0929764 8
Patent No. 6964868
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Garcia, Pablo Dominiguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Giese, Klause
APPLICANT: Randazzo, Filippo
APPLICANT: Kennedy, Giulia C.
APPLICANT: Pot, David
APPLICANT: Kabban, Altaf
APPLICANT: Lamson, George
APPLICANT: Drmanac, Radoje
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana

```
APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, William Lee
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: No. 696486Be1 Human Genes and Gene Expression
TITLE OF INVENTION: Products II
FILE REFERENCE: 2300-1481
CURRENT APPLICATION NUMBER: US/09/297,648
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/072,910
PRIOR FILING DATE: 1998-01-28
PRIOR APPLICATION NUMBER: 60/075,954
PRIOR FILING DATE: 1998-02-24
PRIOR APPLICATION NUMBER: 60/080,666
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/080,515
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/080,114
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/105,234
PRIOR FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 5252
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3922
LENGTH: 745
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(745)
OTHER INFORMATION: n = A,T,C or G
US-09-297-648-3922

Query Match          31.8%;  Score 26.4;  DB 4;  Length 745;
Best Local Similarity  47.5%;  Pred. No. 4.4;
Matches 29;  Conservative 10;  Mismatches 22;  Indels 0;  Gaps 0;

Qy     21 ACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCGAUAUGUGUCUGCCUCAAAAAUCA 80
          |||:|||||:||||| |:.|:: |||.|| |||| |||| || |||||||||||
Db    495 ACAUGAUGGUGACUGUUUUGACAAGUGGNCNAAGCCACAUUGGGAUGCUUCGAAGAGAGA 554

Qy     81 A 81
          |
Db    555 A 555

RESULT 10
US-08-669-408B-9/c
Sequence 9, Application US/0866940BB
Patent No. 6100055
GENERAL INFORMATION:
APPLICANT: GUSS, Bengt
APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: MUELLER, Hans-Peter
APPLICANT: RANTAMAKI, Liisa K.
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING
TITLE OF INVENTION: PLASMAPROTEINASE INHIBITOR-BINDING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
```

```
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,408B
FILING DATE: 03-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00826
FILING DATE: 06-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9302855-3
FILING DATE: 06-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 61743/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1555 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 288..1526
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 288..1526
US-08-669-408B-9

Query Match          31.8%;  Score 26.4;  DB 3;  Length 1555;
Best Local Similarity  35.5%;  Pred. No. 5.8;
Matches 27;  Conservative 18;  Mismatches 31;  Indels 0;  Gaps 0;

Qy      2 CUUGGAGUAAAGUAGCCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCGAUAU 61
          |:|| ||||| :::|||.|| ||| :||| ||||||||||||
Db    891 CUUUACUAGUGCUGCGAGCUUUUAAAGCUUUUCUGUUUUAAAUACGUGUGCUCACUCAUUUU 832

Qy     62 GUGCUGCCUCAAAAU 77
          |:|| :||||||||
Db    831 GAGAUCUUCAAAAAU 816

RESULT 11
US-09-949-016-13209
Sequence 13209, Application US/0994906
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13209
LENGTH: 198942
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(198942)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13209
```

```
Qy          3 UUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUGUGAAAAGGUGCAGGCCAUAUUG 62
              ::||:|:| |||||| |||| ||||:|||||  |:|||| ||  ::||||| ||||||||||||
Db        345 TTTGTGTGACCCACCAGCAAAGAATGGCTTTTGCATTTTAAAAGRGCGGAAAGAAAGAAATG 286

RESULT 13
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
    APPLICANT: Bult et al.
    TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
    TITLE OF INVENTION: jannaschii
    FILE REFERENCE: PB275
    CURRENT APPLICATION NUMBER: US/08/916,421B
    CURRENT FILING DATE: 1997-08-22
    PRIOR APPLICATION NUMBER: US 60/024,428
    PRIOR FILING DATE: 1996-08-22
    NUMBER OF SEQ ID NOS: 3
    SOFTWARE: Patentin version 3.1
    SEQ ID NO 1
    LENGTH: 1664976
    TYPE: DNA
    ORGANISM: Methanococcus jannaschii
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (28222)..(28222)
    OTHER INFORMATION: n equals a, t, c, or g
    NAME/KEY: misc_feature
    LOCATION: (28257)..(28258)
    OTHER INFORMATION: n equals a, t, c, or g
    NAME/KEY: misc_feature
    LOCATION: (84773)..(84773)
```

```
Qy          3 UUGGAGUAAAGUAGCAGCACAUAAUGGUUGUGUGGAUUUUGAAAAGGUGCAGGCCAUAUUG 62
              ::|:|:| |||||| ||||| ||||:|||| |:|||| ||  ::||||| ||||||||||||
Db        141503 TTTGTGTGACCCACCAGCAAAGAATGGCTTTTGCATTTTAAAAGGGGGGAAAGAAAGAATG 141562

RESULT 12
US-09-949-016-50534/c
Sequence 50534, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    FILE REFERENCE: CL001307
    CURRENT APPLICATION NUMBER: US/09/949,016
    CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/241,755
    PRIOR FILING DATE: 2000-10-20
    PRIOR APPLICATION NUMBER: 60/237,768
    PRIOR FILING DATE: 2000-10-03
    PRIOR APPLICATION NUMBER: 60/231,498
    PRIOR FILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 50534
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    TYPE: DNA
    ORGANISM: Human
US-09-949-016-50534
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Best Local Similarity   45.0%;   Pred. No. 35;
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RESULT 14
US-09-692-570-1
Sequence 1, Application US/09692570
US-08-916-421B-1
Patent No. 6797466

Query Match　　　31.1%;　Score 25.8;　DB 3;　Length 1664976;
Best Local Similarity　39.3%;　Pred. No. 1.2e+02;
Matches　24; Conservative　15; Mismatches　22; Indels　0; Gaps　0;

Qy　　22 CAUAUGGUUUGUGAUUUUGAAAAGGUGCAGGCCAUAUUGUGCUCGCUCAAAAUACAA 81
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RESULT 15
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; Sequence 30704, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE:  2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30704
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-30704

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Search completed: November 1, 2006, 22:24:29
Job time : 154.867 secs

Run on: November 1, 2006, 22:20:01 ; Search time 1989.63 seconds
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OM nucleic - nucleic search, using sw model
                 (without alignments)

                 Copyright (c) 1993 - 2006 Biocceleration Ltd.
                 GenCore version 5.1.9

Title: US-10-706-798-1
Perfect score: 83
Sequence: 1 ccuggaguaaaguaguagcagc..........gcugccucaaaauacaagg 83

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 614381638 residues
Total number of hits satisfying chosen parameters: 37784340

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	83	8	US-10-706-798-1	Sequence 1, Appli
2	83	100.0	83	10	US-10-490-955-248	Sequence 248, App
3	83	100.0	83	10	US-10-490-955-305	Sequence 305, App
4	83	100.0	83	15	US-11-100-897-72	Sequence 72, Appl
5	83	100.0	83	16	US-11-230-992-1	Sequence 1, Appli
6	83	100.0	310	10	US-10-909-125-906	Sequence 906, App
7	82	98.8	110	10	US-10-909-125-128	Sequence 128, App
8	82	96.4	110	10	US-10-909-125-165	Sequence 165, App
9	80	74.5	70	10	US-10-909-125-1316	Sequence 1316, Ap
10	61.8	80	8		US-10-706-798-1	Sequence 1, Appli
11	33.4	40.2	83	10	US-10-490-955-248	Sequence 248, App
12	33.4	40.2	83	10	US-10-490-955-305	Sequence 305, App
13	33.4	40.2	83	15	US-11-100-897-72	Sequence 72, Appl
14	33.4	40.2	83	16	US-11-230-992-1	Sequence 1, Appli
15	32.4	40.2	310	10	US-10-909-125-906	Sequence 906, App
16	33.4	39.0	110	10	US-10-909-125-128	Sequence 128, App
17	31	37.3	483	4	US-09-925-065A-615810	Sequence 615810,
18	31	37.3	483	5	US-09-925-065A-615810	Sequence 615810,
19	30.4	36.6	110	10	US-10-909-125-165	Sequence 165, App
20	28.4	34.2	487	6	US-10-027-632-56562	Sequence 56562, A
21	28.4	34.2	487	6	US-10-027-632-316173	Sequence 316173,
22	28.4	34.2	487	7	US-10-027-632-56562	Sequence 56562, A
23	28.4	34.2	487	7	US-10-027-632-316173	Sequence 316173,
24	28.4	34.2	491	6	US-10-027-632-3485	Sequence 3485, Ap
25	28	33.7	491	6	US-10-027-632-3485	Sequence 3485, Ap
26	28	33.7	848	6	US-10-027-632-168106	Sequence 168106,
27	28	33.7	848	6	US-10-027-632-168107	Sequence 168107,
28	28	33.7	848	6	US-10-027-632-168108	Sequence 168108,
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32	28	33.7	848	7	US-10-027-632-168108	Sequence 168108,
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34	28	33.7	1502	7	US-10-437-963-75782	Sequence 75782, A
35	27.8	33.5	617	4	US-09-925-065A-117246	Sequence 117246,
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37	27.8	33.5	623	12	US-10-301-480-216036	Sequence 216036,
38	27.8	33.5	623	12	US-10-301-480-829445	Sequence 829445,
39	27.8	33.5	942	4	US-09-925-065A-283726	Sequence 283726,
40	27.8	33.5	942	5	US-09-925-065A-283726	Sequence 283726,
41	27.6	33.3	4745	8	US-10-607-095-19	Sequence 19, Appl
42	27.6	33.3	312	9	US-10-425-115-139180	Sequence 139180,
43	27.4	33.0	267	8	US-10-282-122A-11092	Sequence 11092, A
44	27.4	33.0	422	12	US-10-301-480-14427	Sequence 14427, A
45	27.4	33.0	422	12	US-10-301-480-627836	Sequence 627836,

ALIGNMENTS

RESULT 1
US-10-706-798-1
; Sequence 1, Application US/10706798
; Publication NO. US20040152112A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: Compositions and Methods for Cancer
; TITLE OF INVENTION: Diagnosis and Therapy
; FILE REFERENCE: 08321-0126US1
; CURRENT APPLICATION NUMBER: US/10/706,798
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 1
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-706-798-1

Query Match   100.0%; Score 83; DB 8; Length 83;
Best Local Similarity   100.0%; Pred. No. 3.3e-19;
Matches   83; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCUUGGAGUAAAGUAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAAGGUCGGCCAUAU 60

Qy   61 UGUGCUGCCUCAAAAUACAAGG 83
          ||||||||||||||||||||||
Db   61 UGUGCUGCCUCAAAAUACAAGG 83

RESULT 2
US-10-490-955-248
; Sequence 248, Application US/10490955

Publication No. US20050059905A1
GENERAL INFORMATION:
APPLICANT: Tuschl, Thomas
APPLICANT: Lagos-Quintana, Mariana
APPLICANT: Lendeckel, Winfried
APPLICANT: Meyer, Jutta
APPLICANT: Rauhut, Reinhard
TITLE OF INVENTION: MicroRNA Molecules
FILE REFERENCE: 2923-613
CURRENT APPLICATION NUMBER: US/10/490,955
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: PCT/EP02/10881
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: EP 01 123 453.1
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 562
SOFTWARE: Patentin version 3.2
SEQ ID NO 248
LENGTH: 83
TYPE: RNA
ORGANISM: Homo sapiens
US-10-490-955-248

```
Query Match         100.0%;  Score 83;  DB 10;  Length 83;
Best Local Similarity  100.0%;  Pred. No. 3.3e-19;
Matches 83;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1  CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGGAGGCCAUAU 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1  CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGGAGGCCAUAU 60

Qy 61  UGUGCUGCCUCAAAAAUACAAGG 83
        |||||||||||||||||||||||
Db 61  UGUGCUGCCUCAAAAAUACAAGG 83
```

RESULT 3
US-10-490-955-305
Sequence 305, Application US/10490955
Publication No. US20050059905A1
GENERAL INFORMATION:
APPLICANT: Tuschl, Thomas
APPLICANT: Lagos-Quintana, Mariana
APPLICANT: Lendeckel, Winfried
APPLICANT: Meyer, Jutta
APPLICANT: Rauhut, Reinhard
TITLE OF INVENTION: MicroRNA Molecules
FILE REFERENCE: 2923-613
CURRENT APPLICATION NUMBER: US/10/490,955
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: EP 02 016 772.2
PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: EP 02 006 712.0
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 02 016 772.2
PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: EP 02 006 712.0
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01 123 453.1
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 562
SOFTWARE: Patentin version 3.2
SEQ ID NO 305
LENGTH: 83
TYPE: RNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: D. melanogaster or H. sapiens or M. musculus or C. elegans or
OTHER INFORMATION: HeLa cells
US-10-490-955-305

RESULT 4
US-11-100-897-72
Sequence 72, Application US/11100897
Publication No. US20050272075A1
GENERAL INFORMATION:
APPLICANT: Jacobsen, Nana
APPLICANT: Kongsbak, Lars
APPLICANT: Kauppinen, Sakari
APPLICANT: Echwald, Soren Morgenthaler
APPLICANT: Mouritzen, Peter
APPLICANT: Nielsen, Peter Stein
APPLICANT: Norholm, Mikkel
TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL INTERFERING RNAS
FILE REFERENCE: 50287/013004
CURRENT APPLICATION NUMBER: US/11/100,897
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/648,221
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 60/619,291
PRIOR FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: 60/600,961
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/590,856
PRIOR FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: 60/560,148
PRIOR FILING DATE: 2004-04-07
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.3
SEQ ID NO 72
LENGTH: 83
TYPE: RNA
ORGANISM: Homo sapiens
US-11-100-897-72

```
Query Match         100.0%;  Score 83;  DB 10;  Length 83;
Best Local Similarity  100.0%;  Pred. No. 3.3e-19;
Matches 83;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1  CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGGAGGCCAUAU 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1  CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGGAGGCCAUAU 60

Qy 61  UGUGCUGCCUCAAAAAUACAAGG 83
        |||||||||||||||||||||||
Db 61  UGUGCUGCCUCAAAAAUACAAGG 83
```

RESULT 5
US-11-230-992-1
Sequence 1, Application US/11230992
Publication No. US20060073505A1
GENERAL INFORMATION:
APPLICANT: Ravi Jain
APPLICANT: Richard H. Griffey
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS EFFECTING DROSHA-MEDIATED CLEAVAGE
FILE REFERENCE: CORE0041US
CURRENT APPLICATION NUMBER: US/11/230,992
CURRENT FILING DATE: 2005-09-20

```
Query Match         100.0%;  Score 83;  DB 15;  Length 83;
Best Local Similarity  100.0%;  Pred. No. 3.3e-19;
Matches 83;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1  CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGGAGGCCAUAU 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1  CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGGAGGCCAUAU 60

Qy 61  UGUGCUGCCUCAAAAAUACAAGG 83
        |||||||||||||||||||||||
Db 61  UGUGCUGCCUCAAAAAUACAAGG 83
```

```
;       PRIOR APPLICATION NUMBER: 60/612,059
;       PRIOR FILING DATE: 2004-09-21
;       NUMBER OF SEQ ID NOS: 54
;       SOFTWARE: FastSEQ for Windows Version 4.0
;
;       SEQ ID NO 1
;       LENGTH: 83
;       TYPE: RNA
;       ORGANISM: H. Sapiens
;
US-11-230-992-1

Qy      CCUUGGAGUAAAGUAGCAGCACAUAAAUGGUUUGUUGGGAUUUUGAAAAAGGUUGCAGGCCCAUAU 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CCUUGGAGUAAAGUAGCAGCACAUAAAUGGUUUGUUGGGAUUUUGAAAAAGGUUGCAGGCCCAUAU 60

Qy   61 UGUGCUGCCUCAAAAAAUACAAGG 83
        |||||||||||||||||||||||
Db   61 UGUGCUGCCUCAAAAAAUACAAGG 83


RESULT 6
US-10-909-125-906
;       Sequence 906, Application US/10909125
;       Publication No. US20050261218A1
;       GENERAL INFORMATION:
;       APPLICANT: Esau, Christine
;       APPLICANT: Lollo, Bridget
;       APPLICANT: Bennett, C. Frank
;       APPLICANT: Freier, Susan M.
;       APPLICANT: Griffey, Richard H.
;       APPLICANT: Baker, Brenda F.
;       APPLICANT: Vickers, Timothy
;       APPLICANT: Marcusson, Eric G.
;       APPLICANT: Koller, Erich
;       APPLICANT: Swayze, Eric
;       APPLICANT: Jain, Ravi
;       APPLICANT: Bhat, Balkrishen
;       APPLICANT: Peralta, Eigen
;       TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
;       FILE REFERENCE: ISIS0080-100 (CORE0016US)
;       CURRENT APPLICATION NUMBER: US/10/909,125
;       CURRENT FILING DATE: 2004-07-30
;       PRIOR APPLICATION NUMBER: US 60/492,056
;       PRIOR FILING DATE: 2003-07-31
;       PRIOR APPLICATION NUMBER: US 60/516,303
;       PRIOR FILING DATE: 2003-10-31
;       PRIOR APPLICATION NUMBER: US 60/531,596
;       PRIOR FILING DATE: 2003-10-31
;       PRIOR APPLICATION NUMBER: US 60/531,596
;       PRIOR FILING DATE: 2003-12-19
;       PRIOR APPLICATION NUMBER: US 60/562,417
;       PRIOR FILING DATE: 2004-04-14
;       NUMBER OF SEQ ID NOS: 2184
;       SOFTWARE: FastSEQ for Windows Version 4.0
;
;       SEQ ID NO 906
;       LENGTH: 310
;       TYPE: DNA
;       ORGANISM: H. sapien
;
US-10-909-125-906

Query Match     100.0%; Score 83; DB 10; Length 310;
Best Local Similarity   73.5%; Pred. No. 5.1e-19;
Matches 61; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

Qy    1 CCUUGGAGUAAAGUAGCAGCACAUAAAUGGUUUGUUGGGAUUUUGAAAAAGGUUGCAGGCCCAUAU 60
        ||||||||||||||||||||||||::||:||||:||||||||||::|||||||||||||||:|||:
Db  131 CCTTGGAGTAGAAGTAGCAGCACACATAATGGTTTGTTGTGGATTTTGAAAAGGTGCAGGCCCATAT 190

Qy   61 UGUGCUGCCUCAAAAAAUACAAGG 83
        :|:||:|||||||||||||||||:
Db  191 TGTGCTGCCTCAAAAATACAAGG 213


RESULT 7
US-10-909-125-128
;       Sequence 128, Application US/10909125
;       Publication No. US20050261218A1
;       GENERAL INFORMATION:
;       APPLICANT: Esau, Christine
;       APPLICANT: Lollo, Bridget
;       APPLICANT: Bennett, C. Frank
;       APPLICANT: Freier, Susan M.
;       APPLICANT: Griffey, Richard H.
;       APPLICANT: Baker, Brenda F.
;       APPLICANT: Vickers, Timothy
;       APPLICANT: Marcusson, Eric G.
;       APPLICANT: Koller, Erich
;       APPLICANT: Swayze, Eric
;       APPLICANT: Jain, Ravi
;       APPLICANT: Bhat, Balkrishen
;       APPLICANT: Peralta, Eigen
;       TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
;       FILE REFERENCE: ISIS0080-100 (CORE0016US)
;       CURRENT APPLICATION NUMBER: US/10/909,125
;       CURRENT FILING DATE: 2004-07-30
;       PRIOR APPLICATION NUMBER: US 60/492,056
;       PRIOR FILING DATE: 2003-07-31
;       PRIOR APPLICATION NUMBER: US 60/516,303
;       PRIOR FILING DATE: 2003-10-31
;       PRIOR APPLICATION NUMBER: US 60/531,596
;       PRIOR FILING DATE: 2003-12-19
;       PRIOR APPLICATION NUMBER: US 60/562,417
;       PRIOR FILING DATE: 2004-04-14
;       NUMBER OF SEQ ID NOS: 2184
;       SOFTWARE: FastSEQ for Windows Version 4.0
;
;       SEQ ID NO 128
;       LENGTH: 110
;       TYPE: RNA
;       ORGANISM: H. sapiens
;
US-10-909-125-128

Query Match     98.8%; Score 82; DB 10; Length 110;
Best Local Similarity   100.0%; Pred. No. 8.3e-19;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    1 CCUUGGAGUAAAGUAGCAGCACAUAAAUGGUUUGUUGGGAUUUUGAAAAAGGUUGCAGGCCCAUAU 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29 CCUUGGAGUAAAGUAGCAGCACAUAAAUGGUUUGUUGGGAUUUUGAAAAAGGUUGCAGGCCCAUAU 88

Qy   61 UGUGCUGCCUCAAAAAAUACAAGG 82
        ||||||||||||||||||||||
Db   89 UGUGCUGCCUCAAAAAAUACAAG 110


RESULT 8
US-10-909-125-165
;       Sequence 165, Application US/10909125
;       Publication No. US20050261218A1
;       GENERAL INFORMATION:
;       APPLICANT: Esau, Christine
;       APPLICANT: Lollo, Bridget
;       APPLICANT: Bennett, C. Frank
;       APPLICANT: Freier, Susan M.
;       APPLICANT: Griffey, Richard H.
;       APPLICANT: Baker, Brenda F.
;       APPLICANT: Vickers, Timothy
;       APPLICANT: Marcusson, Eric G.
;       APPLICANT: Koller, Erich
;       APPLICANT: Swayze, Eric
;       APPLICANT: Jain, Ravi
;       APPLICANT: Bhat, Balkrishen
;       APPLICANT: Peralta, Eigen
;       TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
```

; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 110
; TYPE: RNA
; ORGANISM: H. sapiens
US-10-909-125-165

Query Match 96.4%; Score 80; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCCAUAU 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 31 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCCAUAU 90

Qy 61 UGUGCUGCCUCAAAAAUACA 80
       ||||||||||||||||||||
Db 91 UGUGCUGCCUCAAAAAUACA 110
```

RESULT 9
US-10-909-125-1316
Sequence 1316, Application US/10909125
Publication No. US20050261218A1
GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1316
; LENGTH: 70
; TYPE: RNA
; ORGANISM: Mouse
US-10-909-125-1316

Query Match 74.5%; Score 61.8; DB 10; Length 70;

RESULT 10
US-10-706-798-1/c
Sequence 1, Application US/10706798
Publication No. US20040152112A1
GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: Compositions and Methods for Cancer Diagnosis and Therapy
; FILE REFERENCE: 08321-0126US1
; CURRENT APPLICATION NUMBER: US/10/706,798
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-706-798-1

Query Match 96.9%; Pred. No. 1.1e-11;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 63; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy 11 AAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCCAUAUUGUGCUGCCU 70
       |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db  1 AAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCCCAUAUCUGUGCGCCU 60

Qy 71 CAAAA 75
       |||||
Db 61 CAAAA 65
```

RESULT 11
US-10-490-955-248/c
Sequence 248, Application US/10490955
Publication No. US20050059054A1
GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lagos-Quintana, Mariana
; APPLICANT: Lendeckel, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: Patentin version 3.2

Query Match 40.2%; Score 33.4; DB 8; Length 83;
Best Local Similarity 45.8%; Pred. No. 0.15;
Matches 38; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

```
Qy  1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAAGGUGCAGGCCAUAU 60
       ||:|:||||| |||||  |||||  |||||||||||:|:| :::|||||     |
Db 83 CCTTGTATTTTGAGGCAGCACAAATATGGCCTGCACCTTTCAAAAATCCACAAACCATTA 24

Qy 61 UGUGCUGCCUCAAAAAUACAACAAGG 83
       |:||:|::|:|| | |:||:| | |
Db 23 TGTGCTGCTACTTTACTCCAAGG 1
```

```
; SEQ ID NO 248
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-490-955-248

Query Match       40.2%;  Score 33.4;  DB 10;  Length 83;
Best Local Similarity   45.8%;  Pred. No. 0.15;
Matches 38;  Conservative 14;  Mismatches 31;  Indels 0;  Gaps 0;

Qy    1 CCUGGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUGUGAAAAGGUUGCAGGCCAUAU 60
          ||::||:||   | |||||||||    :::: |||    ||||    ||||
Db   83 CCTTGTATTTTTGAGGCAGCAGCAATATGGCCTGCACCTTTTCAAAAATCCACAAAACCATTA 24

Qy   61 UGUGCCUGCCUCAAAAAAUACAAGG 83
          :|:||:||:||    |||||
Db   23 TGTGCTGCTACTTTACTCCAAGG 1
```

```
RESULT 12
US-10-490-955-305/c
; Sequence 305, Application US10490955
; Publication No. US200505005A1
; GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lagos-Quintana, Mariana
; APPLICANT: Lendeckel, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 305
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: D. melanogaster or H. sapiens or M. musculus or C. elegans or
; OTHER INFORMATION: HeLa cells
US-10-490-955-305

Query Match       40.2%;  Score 33.4;  DB 10;  Length 83;
Best Local Similarity   45.8%;  Pred. No. 0.15;  Mismatches 31;  Indels 0;  Gaps 0;
Matches 38;  Conservative 14;

Qy    1 CCUGGGAGUAAAGUAGCAGCACAUAAAUGGUUGUGUGGAUUUGUGAAAAAGGUUGCAGGGCCAUAU 60
          ||::||:||   | |||||||||    :::: |||    ||||    ||||
Db   83 CCTTGTATTTTTGAGGCAGCACAATATGGCCTGCACCTTTTCAAAAATCCACAAACCATTA 24

Qy   61 UGUGCCUGCCUCAAAAAAUACAAGG 83
          :|:||:||:||    |||||
Db   23 TGTGCTGCTACTTTACTCCAAGG 1
```

```
RESULT 13
US-11-100-897-72/c
; Sequence 72, Application US/11100897
; Publication No. US20050272075A1
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, Nana
; APPLICANT: Kongsbak, Lars
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Echwald, Soren Morgenthaler
; APPLICANT: Mouritzen, Peter
; APPLICANT: Nielsen, Peter Stein
; APPLICANT: Norholm, Mikkel
; TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL
; TITLE OF INVENTION: INTERFERING RNAS
; FILE REFERENCE: 50287/013004
; CURRENT APPLICATION NUMBER: US/11/100,897
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/648,221
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 60/619,291
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/600,961
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/590,856
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/560,148
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 72
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-100-897-72

Query Match       40.2%;  Score 33.4;  DB 15;  Length 83;
Best Local Similarity   45.8%;  Pred. No. 0.15;  Mismatches 31;  Indels 0;  Gaps 0;
Matches 38;  Conservative 14;

Qy    1 CCUGGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUGUGAAAAGGUUGCAGGCCAUAU 60
          ||::||:||   | |||||||||    :::: |||    ||||    ||||
Db   83 CCTTGTATTTTTGAGGCAGCAGCAATATGGCCTGCACCTTTTCAAAAATCCACAAAACCATTA 24

Qy   61 UGUGCCUGCCUCAAAAAAUACAAGG 83
          :|:||:||:||    |||||
Db   23 TGTGCTGCTACTTTACTCCAAGG 1
```

```
RESULT 14
US-11-230-992-1/c
; Sequence 1, Application US/11230992
; Publication No. US20060073505A1
; GENERAL INFORMATION:
; APPLICANT: Ravi Jain
; APPLICANT: Richard H. Griffey
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS EFFECTING
; TITLE OF INVENTION: DROSHA-MEDIATED CLEAVAGE
; FILE REFERENCE: CORE0041US
; CURRENT APPLICATION NUMBER: US/11/230,992
; CURRENT FILING DATE: 2005-09-20
; PRIOR APPLICATION NUMBER: 60/612,059
; PRIOR FILING DATE: 2004-09-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
; LENGTH: 83
; TYPE: RNA
; ORGANISM: H. Sapiens
US-11-230-992-1

Query Match       40.2%;  Score 33.4;  DB 16;  Length 83;
Best Local Similarity   45.8%;  Pred. No. 0.15;  Mismatches 31;  Indels 0;  Gaps 0;
Matches 38;  Conservative 14;

Qy    1 CCUGGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUGUGAAAAGGUUGCAGGCCAUAU 60
          ||::||:||   | |||||||||    :::: |||    ||||    ||||
Db   83 CCTTGTATTTTTGAGGCAGCAGCAATATGGCCTGCACCTTTTCAAAAATCCACAAAACCATTA 24

Qy   61 UGUGCCUGCCUCAAAAAAUACAAGG 83
          :|:||:||:||    |||||
Db   23 TGTGCTGCTACTTTACTCCAAGG 1
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RESULT 15
US-10-909-125-906/c
; Sequence 906, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 906
; LENGTH: 310
; TYPE: DNA
; ORGANISM: H. sapien
US-10-909-125-906

  Query Match   40.2%; Score 33.4; DB 10; Length 310;
  Best Local Similarity   45.8%; Pred. No. 0.23;
  Matches   38; Conservative 14; Mismatches 31; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
              ||:|| | | : | ||||||||| |:| | | :::: ||| ||||||:
Db   213 CCTTGTATTTTTGAGGCAGCACAATATGGCCTGCACCTTTTCAAAATCCACAAACCATTA 154

Qy   61 UGUGCCUGCCUCAAAAAUACAAGG 83
              :|:|||:|:|| ||||| :|||||
Db   153 TGTGCTGCTACTTTACTCCAAGG 131

Search completed: November 2, 2006, 02:46:34
Job time : 1990.63 secs

OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:25:14 ; Search time 187.343 Seconds
               (without alignments)
               859.641 Million cell updates/sec

               GenCore version 5.1.9
               Copyright (c) 1993 - 2006 Biocceleration Ltd.

Title: US-10-706-798-1
Perfect score: 83.
Sequence: 1 ccuggaguaaaguagucagc.........gcugccucaaaaaucaagg 83
Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
Searched: 2461376 seqs, 970166171 residues
Total number of hits satisfying chosen parameters: 4922752
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 45 summaries

Database :   Published Applications NA_New:*
  1: /EMC_Celerra_SID3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
  2: /EMC_Celerra_SID3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
  3: /EMC_Celerra_SID3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
  4: /EMC_Celerra_SID3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
  5: /EMC_Celerra_SID3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
  6: /EMC_Celerra_SID3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
  7: /EMC_Celerra_SID3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
  8: /EMC_Celerra_SID3/ptodata/2/pubpna/US11_NEW_PUB.seq:1
  9: /EMC_Celerra_SID3/ptodata/2/pubpna/US60_NEW_PUB.seq:2
 10: /EMC_Celerra_SID3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	83	8	US-11-194-055-33	Sequence 33, Appl
2	83	100.0	83	9	US-11-375-650-1	Sequence 1, Appli
3	83	100.0	347503	8	US-11-266-748A-23474	Sequence 23474, A
4	79	95.2	108	8	US-11-194-055-325	Sequence 32, Appl
5	40	48.2	108	8	US-11-194-055-325	Sequence 325, App
6	40	48.2	40	8	US-11-194-055-326	Sequence 326, App
7	40	48.2	83	8	US-11-194-055-33	Sequence 33, Appl
8	33.4	40.2	83	9	US-11-375-650-1	Sequence 1, Appli
9	33.4	40.2	347503	8	US-11-266-748A-23474	Sequence 23474, A
c 10	29.6	35.7	108	8	US-11-194-055-32	Sequence 32, Appl
c 11	28	33.7	1313	6	US-11-266-748A-328989	Sequence 328989,
c 12	28	33.7	1385	6	US-10-449-902-2754	Sequence 2754, Ap
c 13	28	33.7	5689	9	US-11-218-305-15422	Sequence 15422, A
c 14	27.4	33.0	333	8	US-11-266-748A-268472	Sequence 268472,
c 15	27.4	33.0	333	8	US-11-194-055-35	Sequence 35, Appl
c 16	27.2	32.8	98	8	US-11-194-055-35	Sequence 35, Appl
c 17	27	32.5	64125	6	US-10-449-902-25833	Sequence 25833, A
c 18	26.8	32.3	3103	6	US-10-539-228-538	Sequence 538, App
c 19	26.8	32.3	39983	6	US-10-539-228-17846	Sequence 17846, A
c 20	26.4	31.8	1502	8	US-11-218-305-17846	Sequence 538, App
c 21	26.4	31.8	181179	8	US-11-266-748A-61130	Sequence 61130, A
c 22	26.2	31.6	810	7	US-11-434-137-9301	Sequence 9301, Ap
c 23	26.2	31.6	810	7	US-11-434-184-9301	Sequence 9301, Ap
c 24	26.2	31.6	810	7	US-11-434-199-9301	Sequence 9301, Ap
c 25	26.2	31.6	810	7	US-11-434-203-9301	Sequence 9301, Ap
c 26	26.2	31.6	813	9	US-11-348-413-7433	Sequence 7433, Ap
c 27	26.2	31.6	228006	6	US-10-540-898-119	Sequence 119, App
c 28	26.2	31.6	2160266	7	US-11-434-137-10967	Sequence 10967, A
c 29	26.2	31.6	2160266	7	US-11-434-184-10967	Sequence 10967, A
c 30	26.2	31.6	2160266	7	US-11-434-199-10967	Sequence 10967, A
c 31	26.2	31.6	2160266	7	US-11-434-203-10967	Sequence 10967, A
c 32	26	31.3	1389	9	US-11-056-355B-1552	Sequence 1552, Ap
c 33	26	31.3	3033	9	US-11-056-355B-6399	Sequence 6399, Ap
c 34	25.8	31.1	2085	7	US-11-218-305-6399	Sequence 6399, Ap
c 35	25.8	31.1	2085	7	US-11-299-286-1012	Sequence 1012, Ap
c 36	25.8	31.1	88208	6	US-10-669-920-909	Sequence 909, App
c 37	25.8	31.1	88445	6	US-10-540-898-497	Sequence 497, App
c 38	25.8	31.1	174600	6	US-11-266-748A-291747	Sequence 291747,
c 39	25.4	30.6	1000	6	US-11-266-748A-343176	Sequence 343176,
c 40	25.4	30.6	1000	8	US-11-266-748A-403264	Sequence 403264,
c 41	25.4	30.6	1000	8	US-11-266-748A-474310	Sequence 474310,
c 42	25.4	30.6	2414	8	US-11-293-697-350	Sequence 350, App
c 43	25.4	30.6	3360	8	US-11-217-529-82548	Sequence 82548, A
c 44	25.4	30.6	82374	8	US-11-266-748A-24977	Sequence 24977, A
c 45	25.4	30.6	82374	8	US-11-266-748A-24977	Sequence 24977, A

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-11-194-055-33
; Sequence 33, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: MicroRNA
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 83
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-33

  Query Match   100.0%; Score 83; DB 8; Length 83;
  Best Local Similarity   73.5%; Pred. No. 1.2e-20;
  Matches   61; Conservative   22; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACACAUAAUGGUUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
Db   1 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTTTGAAAAGGTGCAGGCCATAT 60

Qy   61 UGUGCUGCCUCAAAAAUACAAGG 83

Db
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:|:||:|||:|||||||||||||
61 TGTGCTGCCTCAAAAATACAAGG 83
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RESULT 2
US-11-375-650-1
; Sequence 1, Application US/11375650
; Publication No. US20060165659A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: Compositions and Methods for Cancer
; TITLE OF INVENTION: Diagnosis and Therapy
; FILE REFERENCE: 08321-0126US1
; CURRENT APPLICATION NUMBER: US/11/375,650
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US/10/706,798
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 83
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-375-650-1

Query Match   100.0%; Score 83; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches   83; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCUGGAGUAAAGUACCAGCACAUAAUGGUUUGUGGAUUUUGUGAAAAGGUGCAGGCCCAUAU 60
        ||||||||||||||: |||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCUGGAGUAAAGUAGCACAUAAUGGUUUGUGGAUUUUGUGAAAAGGUGCAGGCCCAUAU 60

Qy 61 UGUGCUGCCUCAAAAAUACAAGG 83
        |||||||||||||||||||||||
Db 61 UGUGCUGCCUCAAAAAUACAAGG 83
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RESULT 3
US-11-266-748A-23474/c
; Sequence 23474, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23474
; LENGTH: 347503
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23474

Query Match   100.0%; Score 83; DB 8; Length 347503;
Best Local Similarity 73.5%; Pred. No. 2.4e-19;
Matches   61; Conservative   22; Mismatches   0; Indels   0; Gaps   0;

```
Qy     1 CCUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGUGAAAAGGUGCAGGCCCAUAU 60
          ||:|||||||||:|||||||||||||::||:||:|||||||||:|||||||||||||||:|:
Db 52198 CCTTGGAGTAAAGTAGCAGCACACATAATGGTTTGTGGATTTTGTGAAAAGGTGCAGGCCCATAT 52139

Qy    61 UGUGCUGCCUCAAAAAUACAAGG 83
          |:|||:|||:|||||||||||||
Db 52138 TGTGCTGCCTCAAAAATACAAGG 52116
```

RESULT 4
US-11-194-055-32
; Sequence 32, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MICRORNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-32

Query Match   95.2%; Score 79; DB 8; Length 108;
Best Local Similarity 72.2%; Pred. No. 3.6e-19;
Matches   57; Conservative   22; Mismatches   0; Indels   0; Gaps   0;

```
Qy   1 CCUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGUGAAAAGGUGCAGGCCCAUAU 60
        ||:|||||||||:|||||||||||::||:||:|||||||||:|||||||||||||||:|:
Db  30 CCTTGGAGTAAAGTAGCAGCACACATAATGGTTTGTGGATTTTGTGAAAAGGTGCAGGCCCATAT 89

Qy  61 UGUGCUGCCUCAAAAAUAC 79
        |:|||:|||:|||||||||
Db  90 TGTGCTGCCTCAAAAATAC 108
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RESULT 5
US-11-194-055-325
; Sequence 325, Application US/11194055

Publication No. US20060105360A1
GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-11-194-055-325

Qy   .

Db   .

Query Match   48.2%; Score 40; DB 8; Length 40;
Best Local Similarity   67.5%; Pred. No. 3.9e-05;
Matches 27; Conservative 13; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACACAUAAUGGUUUGUGGAUUU 40
              ||:|:||||||||||:::|||||||||||||:|:|||||::;
Db   1 CCTTGGAGTAAAGTAGCAGCACATAATGGTTTGTGGATTT 40

RESULT 6
US-11-194-055-326
; Sequence 326, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-11-194-055-326

Query Match   48.2%; Score 40; DB 8; Length 40;
Best Local Similarity   65.0%; Pred. No. 3.9e-05;
Matches 26; Conservative 14; Mismatches   0; Indels   0; Gaps   0;

Qy   30 UUUGUGGAUUUUGAAAAGGUGCAGCCCAUAUUGUGCUGCC 69
              ::||:|:|||||:::||||||||||||||||:|::|||:||
Db   1 TTTGTGGATTTTGAAAAGGTGCAGCCCATATTGTGCTGCC 40

RESULT 7
US-11-055-33/c
; Sequence 33, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George, A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 83
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-194-055-33

Query Match   40.2%; Score 33.4; DB 8; Length 83;
Best Local Similarity   45.8%; Pred. No. 0.013;
Matches 38; Conservative 14; Mismatches 31; Indels   0; Gaps   0;

Qy   1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGAAAAGGUGCAGCCCAUAU 60
              ||:|:||||||:|||||||:||:||::||||||||||||:::::|||||||||||:||||
Db   83 CCTTGTATTTTGAGGCAGCACAATATGGCCTGCACCTTTTCAAAATCCACACAAACCATTA 24

Qy   61 UGUGCUGCCUCAAAAAAUACAAGG 83
              :||:||||||:|:|||||||||||
Db   23 TGTGCTGCTACTTACTCCAAGG 1

RESULT 8
US-11-375-650-1/c
; Sequence 1, Application US/11375650

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; Publication No. US20060165659A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: Compositions and Methods for Cancer
; TITLE OF INVENTION: Diagnosis and Therapy
; FILE REFERENCE: 08321-0126US1
; CURRENT APPLICATION NUMBER: US/11/375,650
; CURRENT FILING DATE: 2006-03-13
; PRIOR APPLICATION NUMBER: US/10/706,798
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 83
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-375-650-1

  Query Match    40.2%;  Score 33.4;  DB 9;  Length 83;
  Best Local Similarity   45.8%;  Pred. No. 0.013;
  Matches   38;  Conservative  14;  Mismatches  31;  Indels   0;  Gaps   0;

Qy     1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
           ||:::|:|| : ||||||||:||||||  ::::  |||| :|||||||||:||||||||:|
Db    83 CCTTGTATTTTTGAGGCAGCACAATATGGCCTGCACCTTTTCAAAATCCACAAACCATTA 24

Qy    61 UGUGCUGCCUCAAAAAUACAAGG 83
           :|:||:||:|| ||||||| ||||
Db    23 TGTGCTGCTACTTTACTCCAAGG 1

RESULT 9
US-11-266-748A-23474
Sequence 23474, Application US/11266748A
; Publication No. US20060134463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 23474
;   LENGTH: 347503
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-23474
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  Query Match    40.2%;  Score 33.4;  DB 8;  Length 347503;
  Best Local Similarity   45.8%;  Pred. No. 0.26;
  Matches   38;  Conservative  14;  Mismatches  31;  Indels   0;  Gaps   0;

Qy        1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGCAGGCCAUAU 60
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Db    52116 CCTTGTATTTTTGAGGCAGCACAATATGGCCTGCACCTTTTCAAAATCCACAAACCATTA 52175

Qy       61 UGUGCUGCCUCAAAAAUACAAGG 83
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Db    52176 TGTGCTGCTACTTTACTCCAAGG 52198

RESULT 10
US-11-194-055-32/c
Sequence 32, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Liu, Chang-Gong
; APPLICANT: Calin, George. A.
; APPLICANT: Cinzia, Sevignani
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
; TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
; TITLE OF INVENTION: FEATURES
; FILE REFERENCE: 3589.1018-008
; CURRENT APPLICATION NUMBER: US/11/194,055
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: PCT/US2005/004865
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/542,940
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,959
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,119
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,929
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/542,963
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/580,797
; PRIOR FILING DATE: 2004-06-18
; NUMBER OF SEQ ID NOS: 663
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 108
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-194-055-32

  Query Match    35.7%;  Score 29.6;  DB 8;  Length 108;
  Best Local Similarity   48.5%;  Pred. No. 0.34;
  Matches   33;  Conservative  11;  Mismatches  24;  Indels   0;  Gaps   0;

Qy    16 GCAGCACAUAAUGGUUUGUGUGGAUUUUGAAAAGGUGCAGGCCAUAUGGCUCAAAA 75
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Db    97 GCAGCACAATATGGCCTGCACCTTTTCAAAATCCACAAACCATTATGTGCTGCTACTTTA 38

Qy    76 AUACAAGG 83
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RESULT 11
US-10-449-902-2754
Sequence 2754, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2754
LENGTH: 1313
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK060554
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-2754

Query Match    33.7%;  Score 28;  DB 6;  Length 1313;
Best Local Similarity  44.7%;
Matches   34;  Conservative  12;  Mismatches  30;  Indels  0;  Gaps  0;

Qy      5 GGAGUAAAGUAGCAGCACAUAAUGGUUUCGUUGGAUUUUGAAAAGGUGCAGGCCAUAUUGUG 64
            |||: |||||| || ||| ::||| ||| :||||||::::||||| |||:|||
Db    330 GAAGTGAAGAAGAAGCAGATTATGCTATTAAGAGATTTGAATATATGATCAAGCTATATGGAA 389

Qy     65 CUGCCUCAAAAAUACA 80
            |||||||:||||:|
Db    390 AACCAATAAGAGTAAA 405
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RESULT 12
US-10-449-902-28048
Sequence 28048, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28048
LENGTH: 1385
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103490
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-28048

Query Match    33.7%;  Score 28;  DB 6;  Length 1385;
Best Local Similarity  44.7%;
Matches   34;  Conservative  12;  Mismatches  30;  Indels  0;  Gaps  0;

Qy      5 GGAGUAAAGUAGCAGCACAUAAUGGUUUCGUUGGAUUUUGAAAAGGUGCAGGCCAUAUUGUG 64
            |||: |||||| || ||| ::||| ||| :||||||::::||||| |||:|||
Db    327 GAAGTGAAGAAGATGCAGATTATGCTATTAAGAGATTTGAATATATGATCAAGCTATATGGAA 386

Qy     65 CUGCCUCAAAAAUACA 80
            |||||||:||||:|
Db    387 AACCAATAAGAGTAAA 402
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RESULT 13
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US-11-218-305-15422/c
Sequence 15422, Application US/11218305
Publication No. US20060141495A1
GENERAL INFORMATION:
APPLICANT: MONSANTO TECHNOLOGY, LLC
APPLICANT: McLaird, Paul L.
APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53660) B
CURRENT APPLICATION NUMBER: US/11/218,305
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 25043
SOFTWARE: Patentin version 3.2
SEQ ID NO 15422
LENGTH: 5689
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (420)..(420)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (759)..(759)
OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-15422

Query Match    33.7%;  Score 28;  DB 9;  Length 5689;
Best Local Similarity  42.6%;
Matches   29;  Conservative  14;  Mismatches  25;  Indels  0;  Gaps  0;

Qy     10 AAAGUAGCAGCACAUAAUGGUUUCGUUGGAUUUUGAAAAGGUGCAGGCCAUAUUGUGUCCUGCC 69
            ||| ||||:|: ||| || ||::||::|||||| :: ||| ||::: | ::|
Db   3570 AAAATATCAGTACAGAACAGTTTGCACATTTGCAGAAAATGAAGACCAGTTTCTTCTGGA 3511

Qy     70 UCAAAAAU 77
            : ||| |:
Db   3510 TTAGAACT 3503
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RESULT 14
US-11-266-748A-268472
Sequence 268472, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
    Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
;
;  SEQ ID NO 268472
;  LENGTH: 333
;  TYPE: DNA
;  ORGANISM: Homo Sapiens
US-11-266-748A-268472

Qy       1 CCUUGGAGUAAAGUAGCAGCACAUAAUGGUUUGUGGAUUUUGUGAAAGGUGCAGGCCAUAU 60
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Db      33 CCUGUGCACACAGUCCCAGCCCUAAUUGGUAUGUGAAUGUUGCACCUUAGCAGCCCAUGT 92

Qy      61 UGUGCUGCC 69
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RESULT 15
US-11-266-748A-328989/c
;  Sequence 328989, Application US/11266748A
;  Publication No. US20060134663A1
;  GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT: Johnston, Patrick
;  APPLICANT: Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION: Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE: 2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105500.7
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
;
;  SEQ ID NO 328989
;  LENGTH: 333
;  TYPE: DNA
;  ORGANISM: Homo Sapiens
US-11-266-748A-328989

Query Match              33.0%;  Score 27.4;  DB 8;  Length 333;
Best Local Similarity    44.9%;  Pred. No. 3.2;
Matches   31;  Conservative   12;  Mismatches   26;  Indels   0;  Gaps   0;

Qy       1 CCUUGGAGUAAAGUAGCAGCACACAUAAUGGUUUGUGGAUUUUGUGAAAGGUGCAGGCCAU 60
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Db     301 CCTGTGCACACAGTCCAGCCCUAAUUGGUAUGUGAAUGUUGCACCUUAGCAGCCCATGT 242

Qy      61 UGUGCUGCC 69
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Query Match   33.0%; Score 27.4; DB 8; Length 333;
Best Local Similarity   44.9%; Pred. No. 3.2;
Matches   31; Conservative   12; Mismatches   26; Indels   0; Gaps   0;

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GenCore version 5.1.9
Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:         November 1, 2006, 19:39:18 ; Search time 487.143 Seconds
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Perfect score:  22
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Scoring table:  IDENTITY_NUC
Sequence:       Gapop 10.0 , Gapext 1.0
Searched:       6366136 seqs, 3197710525 residues
Total number of hits satisfying chosen parameters:  127322272

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl:*
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               13: gb_in:*
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               15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result        %          Query
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  1   22   100.0    22    2   CQ873604    CQ873604 Sequence
  2   22   100.0    22    2   CS166305    CS166305 Sequence
  3   22   100.0    22    2   CS185031    CS185031 Sequence
  4   22   100.0    22    2   CS185033    CS185033 Sequence
  5   22   100.0    22    2   CS185099    CS185099 Sequence
  6   22   100.0    22    2   AJ421733    AJ421733 Homo sapi
  7   22   100.0    22    6   HSA421733   MMU459705 Mus muscu
  8   22   100.0    40    2   MMU459705   AJ459705 Mus muscu
  9   22   100.0    83    2   CS185098    CS185098 Sequence
 10   22   100.0    83    2   CS189094    CS189094 Sequence
 11   22   100.0   108    2   CS188801    CS188801 Sequence
 12   22   100.0   663    5   AY866304    CS188802 Sequence
 13   22   100.0   712    5   AY866308    AY866304 Lemur cat
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 15   22   100.0   825    5   AY866302    AY866306 Pongo pyg
 16   22   100.0   836    5   AY866299    AY866302 Saguinus
 17   22   100.0   871    5   AY866301    AY866299 Ateles ge
 18   22   100.0   896    5   AY866305    AY866301 Macaca ne
 19   22   100.0   901    5   AY866300    AY866305 Macaca mu
 20   22   100.0   902    5   AY866307    AY866300 Gorilla g
 21   22   100.0   914    5   AY866303    AY866307 Pan trogl
 22   22   100.0   153092   5  AC069475    AY866303 Pan panis
 23   22   100.0   154868   5  AF334404    AC069475 Homo sapi
 24   22   100.0   154887   6  AL137060    AF334404 Homo sapi
 25   22   100.0   172152   5  AC154660    AL137060 Human DNA
 26   22   100.0   184155   12 AC155017    AC154660 Mus muscu
 27   22   100.0   235659   12 AC152429    AC155017 Bos tauru
 28   22   100.0   347503   5  AF279660    AC152429 Bos tauru
 29   22   100.0   350000   5  AF440619    AF279660 Homo sapi
 30   22   100.0   945      11 AL607727    AF440619 Homo sapi
 31   20   100.0   157118   5  BX294379    AL607727 Zebrafish
 32   20    90.9   199906   12 AC069286    BX294379 Zebrafish
 33   20    90.9   171118   5  HSA325715   AC069286 Homo sapi
 34   20    90.9   157118   12 AC021764    AJ325715 Homo sapi
 35   19.4   88.2   129986   12 AC148571    AC021764 Homo sapi
 36   19.4   88.2   142102   12 AC149026    AC148571 Taeniopyg
 37   19.4   88.2   145139   12 AC148426    AC149026 Alligator
 38   19.4   88.2   150820   12 AC154053    AC148426 Ornithorh
 39   19.4   88.2   151543   12 AC148422    AC154053 Ictalurus
 40   19.4   88.2   160466   12 AC148572    AC148422 Meleagris
 41   19.4   88.2   161530   12 CT027989    AC148572 Taeniopyg
 42   19.4   88.2   222429   12 AC148419    CT027989 Danio rer
 43   19.4   88.2   250743   11 AB014836    AC148419 Meleagris
 44   19     88.2   161956   11 BX640540    AB014836 Plasmodiu
 45   18.8    85.5   883      5  AF330705    BX640540 Chicken D
                                            AF330705 Homo sapi
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                              ALIGNMENTS

RESULT 1
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LOCUS       CQ873604                  22 bp    RNA      linear  PAT 27-SEP-2004
DEFINITION  Sequence 23 from Patent WO2004076622.
ACCESSION   CQ873604
VERSION     CQ873604.1  GI:52747196
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Taira,K. and Kawasaki,H.
  TITLE     Regulation of mammalian cells
  JOURNAL   Patent: WO 2004076622-A 23 10-SEP-2004;
            National Institute of Advanced Industrial Science and Technology
            (JP)
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"

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  Db          1 TAGCAGCACATAATGGTTTGTG 22


RESULT 2
CS166305

LOCUS       CS166305                  22 bp    RNA      linear  PAT 26-SEP-2005
DEFINITION  Sequence 16 from Patent WO2005078096.
ACCESSION   CS166305
VERSION     CS166305.1  GI:76362075
KEYWORDS    .
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Query Match 100.0%; Score 22; DB 2; Length 22;
Best Local Similarity 68.2%; Pred. No. 1;
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zamore,P.D.
  TITLE     Dual functional oligonucleotides for use in repressing mutant gene
            expression
  JOURNAL   Patent: WO 2005078096-A 16 25-AUG-2005;
            University of Massachusetts (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Db          1 TAGCAGCACATAATGGTTTGTG 22

RESULT 3
CS185031
LOCUS       CS185031                  22 bp    DNA     linear   PAT 01-NOV-2005
DEFINITION  Sequence 5 from Patent WO2005098029.
ACCESSION   CS185031
VERSION     CS185031.1  GI:78585003
KEYWORDS
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jacobsen,N.
  TITLE     NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL INTERFERING
            RNAS
  JOURNAL   Patent: WO 2005098029-A 5 20-OCT-2005;
            Exigon A/S (DK)
FEATURES             Location/Qualifiers
     source          1..22
                     /organism="synthetic construct"
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ORIGIN

Query Match            100.0%;  Score 22;  DB 2;  Length 22;
Best Local Similarity  68.2%;   Pred. No. 1;
Matches   15;  Conservative   7;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :||||||||||:|:||::|:|:|
Db          1 TAGCAGCACATAATGGTTTGTG 22

RESULT 4
CS185033
LOCUS       CS185033                  22 bp    RNA     linear   PAT 01-NOV-2005
DEFINITION  Sequence 7 from Patent WO2005098029.
ACCESSION   CS185033
VERSION     CS185033.1  GI:78585005
KEYWORDS
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jacobsen,N.
  TITLE     NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL INTERFERING
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  JOURNAL   RNAS
            Patent: WO 2005098029-A 7 20-OCT-2005;
            Exigon A/S (DK)
FEATURES             Location/Qualifiers
     source          1..22
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic sequence"
ORIGIN

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :||||||||||:|:||::|:|:|
Db          1 TAGCAGCACATAATGGTTTGTG 22

RESULT 5
CS185099
LOCUS       CS185099                  22 bp    RNA     linear   PAT 01-NOV-2005
DEFINITION  Sequence 73 from Patent WO2005098029.
ACCESSION   CS185099
VERSION     CS185099.1  GI:78585071
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jacobsen,N.
  TITLE     NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL INTERFERING
            RNAS
  JOURNAL   Patent: WO 2005098029-A 73 20-OCT-2005;
            Exigon A/S (DK)
FEATURES             Location/Qualifiers
     source          1..22
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match            100.0%;  Score 22;  DB 2;  Length 22;
Best Local Similarity  68.2%;   Pred. No. 1;
Matches   15;  Conservative   7;  Mismatches   0;  Indels   0;  Gaps   0;

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Db          1 TAGCAGCACATAATGGTTTGTG 22

RESULT 6
HSA421733
LOCUS       HSA421733                 22 bp    RNA     linear   PRI 11-JUN-2003
DEFINITION  Homo sapiens microRNA miR-15.
ACCESSION   AJ421733
VERSION     AJ421733.1  GI:17646018
KEYWORDS    miRNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 22)
  AUTHORS   Lagos-Quintana,M., Rauhut,R., Lendeckel,W. and Tuschl,T.
  TITLE     Identification of novel genes coding for small expressed RNAs
  JOURNAL   Science 294 (5543), 853-858 (2001)
   PUBMED   11679670
REFERENCE   2 (bases 1 to 22)
  AUTHORS   Tuschl,T.
```

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TITLE       Direct Submission
JOURNAL     Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
            Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
            37077, Germany
COMMENT     Related sequences: AC069475.
FEATURES             Location/Qualifiers
     source          1..22
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                     /mol_type="other RNA"
                     /db_xref="taxon:9606"
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                     gene, predicted to form hairpin"
ORIGIN
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            1 TAGCAGCACATAATGGTTTGTG 22

Qy          Query Match         100.0%;  Score 22;  DB 5;  Length 22;
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            Matches   15;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 7
LOCUS       MMU459705                22 bp    mRNA       linear   ROD 05-JUL-2002
DEFINITION  Mus musculus microRNA miR-15a.
ACCESSION   AJ459705
VERSION     AJ459705.1  GI:20799023
KEYWORDS    microRNA miR-15a; miR-15a gene; miRNA.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Lagos-Quintana,M., Rauhut,R., Yalcin,A., Meyer,J., Lendeckel,W. and
            Tuschl,T.
  TITLE     Identification of tissue-specific microRNAs from mouse
  JOURNAL   Curr. Biol. 12 (9), 735-739 (2002)
   PUBMED   12007417
REFERENCE   2  (bases 1 to 22)
  AUTHORS   Tuschl,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAY-2002) Dep. of Cellular Biochemistry, Max Planck
            Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
            37077, Germany
COMMENT     related sequence: TI72137197 (Trace Archive).
FEATURES             Location/Qualifiers
     source          1..22
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
     gene            1..22
                     /gene="miR-15a"
     misc_RNA        1..22
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Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
            1 TAGCAGCACATAATGGTTTGTG 22

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RESULT 8
LOCUS       CS189094                 40 bp    DNA        linear   PAT 04-NOV-2005
DEFINITION  Sequence 325 from Patent WO2005078139.
ACCESSION   CS189094
VERSION     CS189094.1  GI:80750083
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Croce,C.M.
  TITLE     Patent: WO 2005078139-A 325 25-AUG-2005;
  JOURNAL   THOMAS JEFFERSON UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1..40
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide probe"
ORIGIN
Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
             :||||||||||||||||||::||:|
           14 TAGCAGCACATAATGGTTTGTG 35

Qy          Query Match         100.0%;  Score 22;  DB 2;  Length 40;
            Best Local Similarity   68.2%;  Pred. No. 1.1;
            Matches   15;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 9
LOCUS       CS185098                 83 bp    RNA        linear   PAT 01-NOV-2005
DEFINITION  Sequence 72 from Patent WO2005098029.
ACCESSION   CS185098
VERSION     CS185098.1  GI:79585070
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jacobsen,N.
  TITLE     NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL INTERFERING
            RNAS
  JOURNAL   Patent: WO 2005098029-A 72 20-OCT-2005;
            Exiqon A/S (DK)
FEATURES             Location/Qualifiers
     source          1..83
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                     /mol_type="unassigned RNA"
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             :|||||||||||||||||||::||:|
           14 TAGCAGCACATAATGGTTTGTG 35

Qy          Query Match         100.0%;  Score 22;  DB 2;  Length 83;
            Best Local Similarity   68.2%;  Pred. No. 1.2;
            Matches   15;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 10
LOCUS       CS188802                 83 bp    DNA        linear   PAT 04-NOV-2005
DEFINITION  Sequence 33 from Patent WO2005078139.
ACCESSION   CS188802
VERSION     CS188802.1  GI:80749991
KEYWORDS    .
SOURCE      Homo sapiens (human)
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ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
  AUTHORS Croce,C.M.
  JOURNAL Patent: WO 200507813 9-A 33 25-AUG-2005;
    THOMAS JEFFERSON UNIVERSITY (US)
FEATURES   Location/Qualifiers
     source   1..83
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
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Db   14 TAGCAGCACAUAAUGGUUUGUG 35

ORIGIN

Query Match   100.0%; Score 22; DB 2; Length 83;
Best Local Similarity   68.2%; Pred. No. 1.2;
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
CS188801
LOCUS   CS188801   108 bp   DNA   linear   PAT 04-NOV-2005
DEFINITION Sequence 32 from Patent WO200507813 9.
ACCESSION   CS188801
VERSION   CS188801.1 GI:80749790
KEYWORDS
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1
  AUTHORS Croce,C.M.
  JOURNAL Patent: WO 200507813 9-A 32 25-AUG-2005;
    THOMAS JEFFERSON UNIVERSITY (US)
FEATURES   Location/Qualifiers
     source   1..108
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Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
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Db   43 TAGCAGCACAUAAUGGUUUGUG 64

RESULT 12
AY866304
LOCUS   AY866304   663 bp   DNA   linear   PRI 24-JAN-2005
DEFINITION Lemur catta microRNA mir-15a and microRNA mir-16-1 genes, complete
            sequence.
ACCESSION   AY866304
VERSION   AY866304.1 GI:57903106
KEYWORDS
SOURCE   Lemur catta (ring-tailed lemur)
  ORGANISM Lemur catta
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
          Lemuridae; Lemur.
REFERENCE 1 (bases 1 to 663)
  AUTHORS Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
          Plasterk,R.H. and Cuppen,E.
    Phylogenetic Shadowing and Computational Identification of Human

  JOURNAL   microRNA Genes
            Cell 120 (1), 21-24 (2005)
   PUBMED   15652478
REFERENCE 2 (bases 1 to 663)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
            Plasterk,R.H.A. and Cuppen,E.
    TITLE   Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
            3584 CT, The Netherlands
FEATURES   Location/Qualifiers
     source   1..663
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                  /note="based on Homo sapiens mir-15a"
     misc_RNA   463..484
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     misc_RNA   590..663
                  /product="precursor microRNA mir-16-1"
                  /note="based on Homo sapiens mir-16-1"
     misc_RNA   603..624
                  /product="microRNA mir-16-1"

ORIGIN

Query Match   100.0%; Score 22; DB 5; Length 663;
Best Local Similarity   68.2%; Pred. No. 1.6;
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Db   463 TAGCAGCACAUAAUGGUUUGUG 484

RESULT 13
AY866308
LOCUS   AY866308   712 bp   DNA   linear   PRI 24-JAN-2005
DEFINITION Lagothrix lagotricha microRNA mir-15a and microRNA mir-16-1
            genes, complete sequence.
ACCESSION   AY866308
VERSION   AY866308.1 GI:57903110
KEYWORDS
SOURCE   Lagothrix lagotricha
  ORGANISM Lagothrix lagotricha (common woolly monkey)
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
          Cebidae; Atelinae; Lagothrix.
REFERENCE 1 (bases 1 to 712)
  AUTHORS Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
          Plasterk,R.H. and Cuppen,E.
    TITLE Phylogenetic Shadowing and Computational Identification of Human
          microRNA Genes
  JOURNAL Cell 120 (1), 21-24 (2005)
   PUBMED 15652478
REFERENCE 2 (bases 1 to 712)
  AUTHORS Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
          Plasterk,R.H.A. and Cuppen,E.
    TITLE Direct Submission
  JOURNAL Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
          3584 CT, The Netherlands
FEATURES   Location/Qualifiers
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     misc_RNA   403..424
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ORIGIN

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Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
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Db        403 TAGCAGCACATAATGGTTTGTG 424
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RESULT 14

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LOCUS           AY866306     747 bp    DNA    linear   PRI 24-JAN-2005
DEFINITION      Pongo pygmaeus microRNA mir-15a and microRNA mir-16-1 genes,
                complete sequence.
ACCESSION       AY866306
VERSION         AY866306.1   GI:57903108
KEYWORDS        .
SOURCE          Pongo pygmaeus (orangutan)
  ORGANISM      Pongo pygmaeus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Pongo.
REFERENCE       1  (bases 1 to 747)
  AUTHORS       Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
                Plasterk,R.H. and Cuppen,E.
  TITLE         Phylogenetic Shadowing and Computational Identification of Human
                microRNA Genes
  JOURNAL       Cell 120 (1), 21-24 (2005)
   PUBMED       15652478
REFERENCE       2  (bases 1 to 747)
  AUTHORS       Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
                Plasterk,R.H.A. and Cuppen,E.
  TITLE         Direct Submission
  JOURNAL       Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
                3584 CT, The Netherlands
FEATURES             Location/Qualifiers
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ORIGIN

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
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Db        490 TAGCAGCACATAATGGTTTGTG 511
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RESULT 15

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LOCUS           AY866302     825 bp    DNA    linear   PRI 24-JAN-2005
DEFINITION      Saguinus labiatus microRNA mir-15a and microRNA mir-16-1 genes,
                complete sequence.
ACCESSION       AY866302
VERSION         AY866302.1   GI:57903104
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Query Match   100.0%; Score 22; DB 5; Length 712;
Best Local Similarity   68.2%; Pred. No. 1.6;
Matches   15; Conservative   7; Mismatches   0; Indels   0; Gaps   0;

Query Match   100.0%; Score 22; DB 5; Length 747;
Best Local Similarity   68.2%; Pred. No. 1.6;
Matches   15; Conservative   7; Mismatches   0; Indels   0; Gaps   0;

KEYWORDS   .
SOURCE   Saguinus labiatus (red-chested mustached tamarin)
  ORGANISM   Saguinus labiatus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
                Callitrichidae; Saguinus.
REFERENCE   1 (bases 1 to 825)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
                Plasterk,R.H. and Cuppen,E.
  TITLE   Phylogenetic Shadowing and Computational Identification of Human
                microRNA Genes
  JOURNAL   Cell 120 (1), 21-24 (2005)
   PUBMED   15652478
REFERENCE   2 (bases 1 to 825)
  AUTHORS   Berezikov,E., Guryev,V., van de Belt,J., Wienholds,E.,
                Plasterk,R.H.A. and Cuppen,E.
  TITLE   Direct Submission
  JOURNAL   Submitted (29-DEC-2004) Hubrecht Laboratory, Uppsalalaan 8, Utrecht
                3584 CT, The Netherlands
FEATURES   Location/Qualifiers
     source   1..825
                     /organism="Saguinus labiatus"
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                     /note="based on Homo sapiens mir-15a"
     misc_RNA   461..482
                     /product="microRNA mir-15a"
     misc_RNA   588..676
                     /product="precursor microRNA mir-16-1"
                     /note="based on Homo sapiens mir-16-1"
     misc_RNA   601..622
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ORIGIN

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
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Db   461 TAGCAGCACATAATGGTTTGTG 482
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Query Match    100.0%;  Score 22;  DB 5;  Length 825;
Best Local Similarity    68.2%;  Pred. No. 1.6;
Matches    15;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

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OM nucleic - nucleic search, using sw model

                                        GenCore version 5.1.9
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Sequence:         1 uagcagcacauaaugguuugug 22
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Searched:         48236798 seqs, 2795965780 residues
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	22	100.0	638	11	AZ938498	AZ938498 2M0197A08
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c 5	19.4	88.2	627	2	BJ627722	BJ627722 BJ627722
c 6	19.4	88.2	723	9	CX379068	CX379068 JGI_XZT50
c 7	19.4	88.2	785	4	BW723290	BW723290 BW723290
8	19.4	88.2	804	4	BW730170	BW730170 BW730170
9	19.4	88.2	884	3	BU909485	BU909485 AGENCOURT
c 10	19.4	88.5	394	13	CL270436	CL270436 Ggal_105a
c 11	18.8	85.5	586	11	BH048477	BH048477 RPCI-24-3
c 12	18.8	85.5	830	4	CB562036	CB562036 AGENCOURT
c 13	18.8	85.5	893	14	CNS032XX	AL225438 Tetraodon
c 14	18.4	83.6	348	10	DR975958	DR975958 Skin-13_B
c 15	18.4	83.6	932	1	AL694787	AL694787 AL694787
c 16	17.8	80.9	191	7	AI633347	AI633347 t896b02.x
17	17.8	80.9	386	11	AQ892377	AQ892377 HS_3112_B
18	17.8	80.9	421	11	AQ186977	AQ186977 HS_3122_B
c 19	17.8	80.9	422	8	CX082256	CX082256 EHAAT87TR
c 20	17.8	80.9	473	8	CV473806	CV473806 22089.1 D
21	17.8	80.9	599	8	CX088035	CX088035 EHADA56TR
22	17.8	80.9	604	8	CX089370	CX089370 EHADX37TR
c 23	17.8	80.9	613	14	DE135052	DE135052 Oryzias_l
c 24	17.8	80.9	617	13	CZ078834	CZ078834 OM_Ba007
c 25	17.8	80.9	631	8	CX097110	CX097110 EHAHI9STR
c 26	17.8	80.9	670	14	CR061257	CR061257 Reverse 8
c 27	17.8	80.9	679	11	AZ428541	AZ428541 1M0212005
c 28	17.8	80.9	764	13	DU452257	DU452257 10984210G
c 29	17.8	80.9	802	4	BX887642	BX887642 BX887642
c 30	17.8	80.9	804	13	CW837931	CW837931 GT9326.Db3
c 31	17.8	80.9	823	11	BH161771	BH161771 ENTRC17TF
c 32	17.8	80.9	860	11	AZ678560	AZ678560 ENTMS1STF
c 33	17.8	80.9	889	11	AZ684626	AZ684626 ENTKU65TF
c 34	17.8	80.9	983	11	BH164645	BH164645 ENTQV72TF
c 35	17.8	80.9	1272	8	BI869305	BI869305 603396203
c 36	17.4	79.1	260	13	CW401759	CW401759 f8bb001f0
37	17.4	79.1	271	4	BX688587	BX688587 BX688587
38	17.4	79.1	364	12	CE710553	CE710553 tigr-988-
c 39	17.4	79.1	412	12	CB617339	CB617339 EST14_Oy
c 40	17.4	79.1	420	1	AL119702	AL119702 DKFZp7610
c 41	17.4	79.1	459	3	BP085372	BP085372 BP085372
c 42	17.4	79.1	500	1	AU086235	AU086235 AU086235
43	17.4	79.1	543	2	BG410941	BG410941 EM1_27_H0
44	17.4	79.1	611	11	BH059786	BH059786 RPCI-24-3
c 45	17.4	79.1	627	13	CW112106	CW112106 RPCI_104_485_1

ALIGNMENTS

RESULT 1
DR22A19S

```
LOCUS       DR22A19S              330 bp    DNA     linear   GSS 27-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-22A19, genomic survey sequence.
ACCESSION   AL739377
VERSION     AL739377.1  GI:21348782
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 330)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 22A19. 22A19 is
            part of the Daniokey BAC library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1..330
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-22A19"
                     /tissue_type="Testis"
                     /note="Vector pIndigoBAC-536"
ORIGIN
```

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Query Match            100.0%;  Score 22;  DB 14;  Length 330;
Best Local Similarity   68.2%;
Matches   15;  Conservative  7;  Mismatches  6;  Pred. No. 6.6;  Indels  0;  Gaps  0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              ||||||||||| ||:||:||:|
Db        162 TAGCAGCACATAATGGTTTGTG 183
```

RESULT 2

```
LOCUS       AQ672199              486 bp    DNA     linear   GSS 24-JUN-1999
DEFINITION  HS_2151_B1_B12_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2151 Col=23 Row=D, genomic survey
            sequence.
ACCESSION   AQ672199
VERSION     AQ672199.1  GI:5204870
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            University of Washington
            High Throughput Sequencing Center
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 2151 row: D column: 23
            Seq primer: M13 Reverse
            Class: BAC ends
            High quality sequence stop: 486.
FEATURES             Location/Qualifiers
     source          1..486
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=2151 Col=23 Row=D"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-coli DH10B"
ORIGIN

Query Match             100.0%;  Score 22;  DB 11;  Length 486;
  Best Local Similarity   68.2%;          Pred. No. 6.9;
  Matches 15;  Conservative  7;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              |||||||||||:||:|||||||
Db        427 TAGCAGCACAUAAUUGGUUUGUG 406
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```
RESULT 3
LOCUS       AZ938498              638 bp    DNA     linear   GSS 26-APR-2001
DEFINITION  2M0197A08F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0197A08 F, genomic survey sequence.
ACCESSION   AZ938498
VERSION     AZ938498.1  GI:13798291
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 638)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 7177
            Fax: 801 585 5606
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0197  row: A  column: 08
            Seq primer: CGTTGTPAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1..638
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0197A08"
                     /sex="female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1|), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

Query Match             100.0%;  Score 22;  DB 11;  Length 638;
  Best Local Similarity   68.2%;          Pred. No. 7.1;
  Matches 15;  Conservative  7;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              |||||||||||:||:|||||||
Db        188 TAGCAGCACAUAAUGGUUUGUG 167
```

```
RESULT 4
LOCUS       BW837082              445 bp    mRNA    linear   EST 24-DEC-2005
DEFINITION  BW837082 Amphioxus Branchiostoma floridae unpublished cDNA library,
            larva whole animal Branchiostoma floridae cDNA clone bflv059118 3',
            mRNA sequence.
ACCESSION   BW837082
VERSION     BW837082.1  GI:66445298
KEYWORDS    EST.
SOURCE      Branchiostoma floridae (Florida lancelet)
  ORGANISM  Branchiostoma floridae
            Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
            Branchiostoma.
REFERENCE   1  (bases 1 to 445)
  AUTHORS   Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
  TITLE     Expressed genes in Branchiostoma floridae
  JOURNAL   Unpublished (2005)

Query Match             100.0%;  Score 22;  DB 11;  Length 445;
  Best Local Similarity   68.2%;          Pred. No. 7.1;
  Matches 15;  Conservative  7;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              |||||||||||:||:|||||||
Db        188 TAGCAGCACAUAAUGGUUUGUG 167
```

COMMENT   Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshin@genes.nig.ac.jp
            If you want to have a cDNA clone for this EST or if you have any
            questions, please send an e-mail to Nori Satoh
            (satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
            (yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES   source
            /organism="Branchiostoma floridae"
            /mol_type="mRNA"
            /clone="bflv059i18"
            /db_xref="taxon:7739"
            /tissue_type="whole animal"
            /dev_stage="larva"
            /clone_lib="Amphioxus Branchiostoma floridae unpublished
            cDNA library, larva whole animal"
ORIGIN
            1   ..445

Qy   Query Match   88.2%;   Score 19.4; DB 4; Length 445;
     Best Local Similarity 66.7%; Pred. No. 1.4e+02;
     Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy   2 AGCAGGACACAUAAUGGUUUGUG 22
         ||||| |||||||||||||||:||
Db   56 AGCAGUACAUAAUGGUUUGUG 76

RESULT 5
LOCUS   BJ627722   627 bp   mRNA   linear   EST 01-OCT-2003
DEFINITION BJ627722 NIBB Mochii normalized Xenopus early gastrula library
            Xenopus laevis cDNA clone XL219c06 5', mRNA sequence.
ACCESSION   BJ627722
VERSION   BJ627722.1 GI:37274592
KEYWORDS   EST.
SOURCE   Xenopus laevis (African clawed frog)
  ORGANISM Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1 (bases 1 to 627)
  AUTHORS   Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,Y.
  TITLE   Expressed genes in X. laevis embryo
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshin@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.
FEATURES   source
            1   ..627
            /organism="Xenopus laevis"
            /mol_type="mRNA"
            /db_xref="taxon:8355"
            /clone="XL219c06"
            /tissue_type="whole embryo"
            /dev_stage="stage 10.5"
            /clone_lib="NIBB Mochii normalized Xenopus early gastrula
            library"
ORIGIN

Qy   Query Match   88.2%;   Score 19.4; DB 2; Length 627;

Best Local Similarity 61.9%; Pred. No. 1.4e+02;
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 21
         ||||||||||||:|||::|:|:
Db 200 TAGCAGCACATACATGGTTTGT 220

RESULT 6
LOCUS   CX379068   723 bp   mRNA   linear   EST 08-SEP-2005
DEFINITION CX379068 JGI XZT50833.fwd NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone
            IMAGE:7625775 5', mRNA sequence.
ACCESSION   CX379068
VERSION   CX379068.2 GI:74290621
KEYWORDS   EST.
SOURCE   Xenopus tropicalis (western clawed frog)
  ORGANISM Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1 (bases 1 to 723)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
  TITLE   DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT   On Jan 5, 2005 this sequence version replaced gi:57147625.
            Contact: Lindquist,B.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Distribution: I.M.A.G.E. Consortium/LLNL:
            http://image.llnl.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
            indicates a forward sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Plate: XZT 0529 row: b column: 13
            High quality sequence stop: 668.
FEATURES   source
            1   ..723
            /organism="Xenopus tropicalis"
            /mol_type="mRNA"
            /db_xref="taxon:8364"
            /clone="IMAGE:7625775"
            /tissue_type="whole embryo"
            /dev_stage="Tadpole (st. 36-41)"
            /lab_host="E. coli XL1-Blue derivative, Stratagene
            ElectroTen-Blue"
            /clone_lib="NIH_XGC_tropTad5"
            /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
            library constructed by Russell B. Fletcher in R. Harland's
            lab using poly A RNA and oligo dT primers (Invitrogen
            SuperScript Plasmid System for cDNA Synthesis and
            Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
            into vector pCS108
            (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
            ."
ORIGIN

Qy   Query Match   88.2%;   Score 19.4; DB 9; Length 723;
     Best Local Similarity 61.9%; Pred. No. 1.5e+02;
     Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy   1 UAGCAGCACAUAAUGGUUUGU 21
         ||||||||||| |:|||::|::|:

Db　　175 TAGCAGCACATCATGGTTTGT 195

RESULT 7
BW723290
LOCUS　　　BW723290　　785 bp　　mRNA　　linear　　EST 22-OCT-2005
DEFINITION　BW723290 Amphioxus Branchiostoma floridae unpublished cDNA library,
　　　　　　adult whole animal Branchiostoma floridae cDNA clone bfad035b06 3',
　　　　　　mRNA sequence.
ACCESSION　BW723290
VERSION　　BW723290.1　GI:66309882
KEYWORDS　　EST.
SOURCE　　Branchiostoma floridae (Florida lancelet)
ORGANISM　　Branchiostoma floridae
　　　　　　Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
　　　　　　Branchiostoma.
REFERENCE　1　(bases 1 to 785)
AUTHORS　　Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
TITLE　　　Expressed genes in Branchiostoma floridae
JOURNAL　　Unpublished (2005)
COMMENT　　Contact: Tadasu Shin-i
　　　　　　National Institute of Genetics
　　　　　　Center For Genetic Resource Information
　　　　　　1111 Yata, Mishima, Shizuoka 411-8540, Japan
　　　　　　Tel: 81-559-81-6856
　　　　　　Fax: 81-559-81-6855
　　　　　　Email: tshini@genes.nig.ac.jp
　　　　　　If you want to have a cDNA clone for this EST or if you have any
　　　　　　questions, please send an e-mail to Nori Satoh
　　　　　　(satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
　　　　　　(yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES　　　　　Location/Qualifiers
source　　　1..785
　　　　　　/organism="Branchiostoma floridae"
　　　　　　/mol_type="mRNA"
　　　　　　/db_xref="taxon:7739"
　　　　　　/clone="bfad035b06"
　　　　　　/tissue_type="whole animal"
　　　　　　/dev_stage="adult"
　　　　　　/clone_lib="Amphioxus Branchiostoma floridae unpublished
　　　　　　cDNA library, adult whole animal"
ORIGIN
Qy　　2 AGCAGCACAUAAUGGUUUGUG 22
　　　　　|||||:|||||:||:|||||:|
Db　　63 AGCAGTACATAARGGTTTGTG 83

Query Match　88.2%;　Score 19.4;　DB 4;　Length 785;
Best Local Similarity　66.7%;　Pred. No. 1.5e+02;
Matches　14;　Conservative　6;　Mismatches　1;　Indels　0;　Gaps　0;

RESULT 8
BW730170
LOCUS　　　BW730170　　804 bp　　mRNA　　linear　　EST 22-OCT-2005
DEFINITION　BW730170 Amphioxus Branchiostoma floridae unpublished cDNA library,
　　　　　　adult whole animal Branchiostoma floridae cDNA clone bfad054g14 3',
　　　　　　mRNA sequence.
ACCESSION　BW730170
VERSION　　BW730170.1　GI:66316782
KEYWORDS　　EST.
SOURCE　　Branchiostoma floridae (Florida lancelet)
ORGANISM　　Branchiostoma floridae
　　　　　　Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
　　　　　　Branchiostoma.
REFERENCE　1　(bases 1 to 804)
AUTHORS　　Yu,J., Holland,L.Z., Shin-i,T., Kohara,Y., Satou,Y. and Satoh,N.
TITLE　　　Expressed genes in Branchiostoma floridae
JOURNAL　　Unpublished (2005)
COMMENT　　Contact: Tadasu Shin-i
　　　　　　National Institute of Genetics
　　　　　　Center For Genetic Resource Information
　　　　　　1111 Yata, Mishima, Shizuoka 411-8540, Japan
　　　　　　Tel: 81-559-81-6856
　　　　　　Fax: 81-559-81-6855
　　　　　　Email: tshini@genes.nig.ac.jp
　　　　　　If you want to have a cDNA clone for this EST or if you have any
　　　　　　questions, please send an e-mail to Nori Satoh
　　　　　　(satoh@ascidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou
　　　　　　(yutaka@ascidian.zool.kyoto-u.ac.jp).
FEATURES　　　　　Location/Qualifiers
source　　　1..804
　　　　　　/organism="Branchiostoma floridae"
　　　　　　/mol_type="mRNA"
　　　　　　/db_xref="taxon:7739"
　　　　　　/clone="bfad054g14"
　　　　　　/tissue_type="whole animal"
　　　　　　/dev_stage="adult"
　　　　　　/clone_lib="Amphioxus Branchiostoma floridae unpublished
　　　　　　cDNA library, adult whole animal"
ORIGIN
Qy　　2 AGCAGCACAUAAUGGUUUGUG 22
　　　　　|||||:|||||:||:|||||:|
Db　　66 AGCAGTACATAARGGTTTGTG 86

Query Match　88.2%;　Score 19.4;　DB 4;　Length 804;
Best Local Similarity　66.7%;　Pred. No. 1.5e+02;
Matches　14;　Conservative　6;　Mismatches　1;　Indels　0;　Gaps　0;

RESULT 9
BU909485
LOCUS　　　BU909485　　884 bp　　mRNA　　linear　　EST 17-OCT-2002
DEFINITION　AGENCOURT_10481253 NICHD_XGC_Emb1 Xenopus laevis cDNA clone
　　　　　　IMAGE:6635141 5', mRNA sequence.
ACCESSION　BU909485
VERSION　　BU909485.1　GI:24091399
KEYWORDS　　EST.
SOURCE　　Xenopus laevis (African clawed frog)
ORGANISM　　Xenopus laevis
　　　　　　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
　　　　　　Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
　　　　　　Xenopodinae; Xenopus; Xenopus.
REFERENCE　1　(bases 1 to 884)
AUTHORS　　Klein,S., Gerhard,D., Wagner,L., Richardson,P., Schriml,L.,
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE　　　National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
　　　　　　Tumor Gene Index
JOURNAL　　Unpublished (1997)
COMMENT　　Contact: Robert Strausberg, Ph.D.
　　　　　　Email: cgapbs-r@mail.nih.gov
　　　　　　Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
　　　　　　cDNA Library Preparation: Life Technologies, Inc.
　　　　　　cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
　　　　　　DNA Sequencing by: Agencourt Bioscience Corporation
　　　　　　Clone distribution: NCI-CGAP clone distribution information can be
　　　　　　found through the I.M.A.G.E. Consortium/LLNL at:
　　　　　　http://image.llnl.gov
　　　　　　Plate: LLAM14208　row: n　column: 05
　　　　　　High quality sequence stop: 633.
FEATURES　　　　　Location/Qualifiers
source　　　1..884
　　　　　　/organism="Xenopus laevis"
　　　　　　/mol_type="mRNA"
　　　　　　/db_xref="taxon:8355"
　　　　　　/clone="IMAGE:6635141"
　　　　　　/tissue_type="embryo (stage 10)"
　　　　　　/lab_host="DH10B (phage-resistant)"
　　　　　　/clone_lib="NICHD_XGC_Emb1"
　　　　　　/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
　　　　　　Cloned unidirectionally. Primer: Oligo dT. Average insert
　　　　　　size 1.55 kb. Constructed by Life Technologies. Note: This
　　　　　　is a Xenopus Gene Collection (XGC) library."
ORIGIN
Query Match　88.2%;　Score 19.4;　DB 3;　Length 884;

RESULT 10

Best Local Similarity 61.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy   1 UAGCAGCCACAUAAUGGUUUGU 21
         :||||||||| |:|:||:::|:
Db   185 TAGCAGCCATCATCGGTTTGT 205

LOCUS   CL270436/c
DEFINITION CL270436   394 bp   DNA   linear GSS 08-FEB-2005
            Ggal_105a_PR_B06 Ggal_PR-1 Gallus gallus genomic clone
ACCESSION   CL270436
VERSION   CL270436.1 GI:58747778
KEYWORDS   GSS.
SOURCE   Gallus gallus (chicken)
  ORGANISM Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1 (bases 1 to 394)
  AUTHORS   Wicker,T., Robertson,J.S., Schulze,S.R., Feltus,F.A., Magrini,V.,
            Morrison,J.A., Mardis,E.R., Wilson,R.K., Peterson,D.G.,
            Paterson,A.H. and Ivarie,R.
  TITLE   The repetitive landscape of the chicken genome
  JOURNAL   Genome Res. 15 (1), 126-136 (2005)
   PUBMED   15525510
COMMENT   Contact: Paterson AH
            Plant Genome Mapping Laboratory
            University of Georgia, Center for Applied Genetic Technologies
            Riverbend Research Laboratory, Room 162, 110 Riverbend Road,
            Athens, GA 30602 USA
            Tel: 7065830169
            Fax: 7065830160
            Email: paterson@uga.edu
            Sequence from middle repetitive (MR) Cot fraction, Cot 10-100
            Class: Hydroxyapatite-fractionated DNA.
FEATURES   Location/Qualifiers
     source   1..394
                     /organism="Gallus gallus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9031"
                     /clone="Ggal_105a_PR_B06"
                     /sex="female"
                     /clone_lib="Ggal_PR-1"
                     /note="produced by Cot-based cloning and sequencing
                     (CBCS)"
ORIGIN

RESULT 11

Query Match   85.5%; Score 18.8; DB 13; Length 394;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy   1 UAGCAGCCACAUAAUGGUUUGUG 22
         :|| |||||| ||||::||::|:|
Db   170 TAGAAGCCACAGAATGGTTTGTG 149

LOCUS   BH048477/c
DEFINITION BH048477   586 bp   DNA   linear GSS 17-JUL-2001
            RPCI-24-346O15.TV RPCI-24 Mus musculus genomic clone
ACCESSION   RPCI-24-346O15, genomic survey sequence.
VERSION   BH048477
            BH048477.1 GI:14836401
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 586)

AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akhiret,B., Levins,M.,
            Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE   Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Other GSSs: RPCI-24-346O15.TJ
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 346 row: O column: 15
            Seq primer: T7
            Class: BAC ends.
FEATURES   Location/Qualifiers
     source   1..586
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-346O15"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /clone_lib="RPCI-24"
                     /note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1.
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI partially digested male C57BL/6J
                     DNA."
ORIGIN

RESULT 12

Query Match   85.5%; Score 18.8; DB 11; Length 586;
Best Local Similarity 59.1%; Pred. No. 2.9e+02;
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy   1 UAGCAGCCACAUAAUGGUUUGUG 22
         :||||| |||||||::||::|:|
Db   321 TAACAGCATATAAATGGTTTGTG 300

LOCUS   CB562036
DEFINITION CB562036   830 bp   mRNA   linear EST 02-APR-2003
            AGENCOURT1 13324904 NICHD_XGC Tad1 Xenopus laevis cDNA clone
            IMAGE:6880576 3', mRNA sequence.
ACCESSION   CB562036
VERSION   CB562036.1 GI:29481566
KEYWORDS   EST.
SOURCE   Xenopus laevis (African clawed frog)
  ORGANISM Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1 (bases 1 to 830)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbc-r@mail.nih.gov
            Tissue Procurement: Drs. Donald Brown and Liquan Cai
            cDNA Library Preparation: CLONTECH
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES
    source
        /organism="Xenopus laevis"
        /mol_type="mRNA"
        /db_xref="taxon:8355"
        /clone="IMAGE:6880576"
        /clone_lib="NICHD_XGC_Tad1"
        /dev_stage="metamorphosis stage 53"
        /note="Organ: Developing Tadpole; Vector: pDNR-LIB;
        Site.1: Sfi; Site.2: Sfi; 5' and 3' adaptors were used in
        cloning as follows: 5' adaptor sequence:
        5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
        5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
        C, or G and N = A, C, G, or T). Average insert size 1.6 kb
        (range 0.9-3.0 kb). 15/15 colonies contained inserts by
        PCR. This library was enriched for full-length clones and
        was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
            ||||| |||||:||||:|||||
Db   336 TTGCAGCTCATTAATGGTTTGTG 357

Query Match   85.5%; Score 18.8; DB 4; Length 830;
Best Local Similarity 59.1%; Pred. No. 3e+02;
Matches   13; Conservative   7; Mismatches   2; Indels   0; Gaps   0;

RESULT 13
CNS032XX
LOCUS   CNS032XX   893 bp   DNA   linear   GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
            207L24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL225438
VERSION   AL225438.1 GI:7884333
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 893)
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE   Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE   Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  PUBMED   1089143
REFERENCE   3 (bases 1 to 893)
  JOURNAL   Direct Submission
            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT   This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
    source   1. .893
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="207L24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG207DF12LP1
                     end : T7"

ORIGIN

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
            |||||||||||:|||| :|||||
Db   631 TAGCAGCACGGAATGGTTTGTG 652

Query Match   85.5%; Score 18.8; DB 14; Length 893;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches   14; Conservative   6; Mismatches   2; Indels   0; Gaps   0;

RESULT 14
DR975958
LOCUS   DR975958   348 bp   mRNA   linear   EST 03-JAN-2006
DEFINITION Skin-13_B03_pDNR-LIB-SF11A A. transmontanus skin express library
            Acipenser transmontanus cDNA, mRNA sequence.
ACCESSION   DR975958
VERSION   DR975958.1 GI:84178869
KEYWORDS   EST.
SOURCE   Acipenser transmontanus (white sturgeon)
  ORGANISM Acipenser transmontanus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
            Acipenser.
REFERENCE   1 (bases 1 to 348)
  AUTHORS   Mariani,V., Malinverni,R. and Giuffra,E.
  TITLE   Transcriptome analysis of the American sturgeon (Acipenser
            transmontanus): pathways of gene expression in the spleen and skin
  JOURNAL   Unpublished (2005)
COMMENT   Contact: Valentina Mariani
            Livestock Genomics 1
            PTP-CERSA
            Via Einstein, Loc. Ca. na Codazza, 26900 Lodi (LO), Italy
            Email: valentina.mariani@tecnoparco.org.
FEATURES   Location/Qualifiers
    source   1. .348
                     /organism="Acipenser transmontanus"
                     /mol_type="mRNA"
                     /db_xref="taxon:7904"
                     /clone_lib="A. transmontanus skin express library"
                     /note="Organ: skin"

ORIGIN

Qy   1 UAGCAGCACAUAAUGGUUUGUG 20
            |||||||||||:|:|||:|||:|
Db   229 TAGCAGCACATCATGGTTTTG 210

Query Match   83.6%; Score 18.4; DB 10; Length 348;
Best Local Similarity 65.0%; Pred. No. 4.3e+02;
Matches   13; Conservative   6; Mismatches   1; Indels   0; Gaps   0;

RESULT 15
AL694787/c
LOCUS   AL694787   932 bp   mRNA   linear   EST 21-MAR-2002
DEFINITION AL694787 NAP1 Anopheles gambiae cDNA clone NAP1-P23-F-06-5, mRNA
            sequence.
ACCESSION   AL694787
VERSION   AL694787.1 GI:19614493
KEYWORDS   EST.
SOURCE   Anopheles gambiae (African malaria mosquito)
  ORGANISM Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.

REFERENCE   1 (bases 1 to 932)
AUTHORS   Christophides,G.K., Blass,K., Zdobnov,E.M., Carmouche,R., Benes,V.
            and Kafatos,F.C.
TITLE   Anopheles gambiae EST, European Molecular Biology Laboratory
JOURNAL   Unpublished (2002)
COMMENT   Contact: Christophides GK
            Fotis C. Kafatos laboratory
            European Molecular Biology Laboratory
            Meyerhofstrasse 1, 69117 Heidelberg, Germany
            Tel: +49 6221 387-440
            Fax: +49 6221 387-306
            Email: christop@embl-heidelberg.de
            Plate: P23 row: F column: 06.
FEATURES   Location/Qualifiers
     source   1..932
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /db_xref="taxon:7165"
                     /clone="NAP1-P23-F-06-5"
                     /lab_host="E. coli DH10B"
                     /clone_lib="NAP1"
                     /note="Vector: pT7T3D-PacI; Site_1: NotI; Site_2: EcoRI;
                     ESTs sequenced from the T7 priming site that reads from
                     the 5' end of cDNA. The NAP1 is a directionally cloned and
                     normalized, oligo-T primed cDNA library constructed from a
                     mixture of Anopheles gambiae developmental stages
                     according to: Bonaldo, Lennon & Soares (1996):
                     Normalization and Subtraction: Two Approaches To
                     Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN

Query Match   83.6%; Score 18.4; DB 1; Length 932;
Best Local Similarity   65.0%; Pred. No. 4.8e+02;
Matches   13; Conservative   6; Mismatches   1; Indels   0; Gaps   0;

Qy   2 AGCAGCACAUAAUGGUUUGU 21
        |||||||||||:|:||:::|:
Db 297 AGCAGCCACATATTGGTTTGT 278

Search completed: November 1, 2006, 22:21:01
Job time : 1026.17 secs

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OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: November 1, 2006, 19:02:55 ; Search time 105.39 Seconds
(without alignments)
1455.440 Million cell updates/sec

Title: US-10-706-798-3
Perfect score: 22
Sequence: 1 uagcagcacauaaugguuguug 22
Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :
  N_Geneseq_8:*
   1: geneseqn1980s:*
   2: geneseqn1990s:*
   3: geneseqn2000s:*
   4: geneseqn2001s:*
   5: geneseqn2001bs:*
   6: geneseqn2002as:*
   7: geneseqn2002bs:*
   8: geneseqn2003as:*
   9: geneseqn2003bs:*
  10: geneseqn2003cs:*
  11: geneseqn2004ds:*
  12: geneseqn2004bs:*
  13: geneseqn2004s:*
  14: geneseqn2005s:*
  15: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	22	100.0	22	8	ADA00084	Ada00084 Human miR
2	22	100.0	22	8	ADA00122	Ada00122 Mouse miR
3	22	100.0	22	12	ADO17091	Ado17091 Human miR
4	22	100.0	22	12	ADP84065	Adp84065 Small nuc
5	22	100.0	22	13	ADR83121	Adr83121 Human miR
6	22	100.0	22	14	ADX03284	Adx03284 Antisense
7	22	100.0	22	14	ADX03184	Adx03184 Human mic
8	22	100.0	22	14	ADY30915	Ady30915 Micro RNA
9	22	100.0	22	14	ADX85423	Adx85423 Human/mou
10	22	100.0	22	14	ADZ20390	Adz20390 Human hem
11	22	100.0	22	14	AEC36205	Aec36205 Nucleotid
12	22	100.0	22	14	AED35921	Aed35921 Hsa-miR-1
13	22	100.0	22	14	AED35925	Aed35925 Hsa-miR-1
14	22	100.0	22	14	AED35991	Aed35991 Human mic
15	22	100.0	22	14	AED53385	Aed53385 Human mic
16	22	100.0	22	14	AED53470	Aed53470 Mouse tar
17	22	100.0	22	14	AEO43383	Aeo43383 Mouse mir
18	22	100.0	22	14	AEO04287	Aee04287 Human mir
19	22	100.0	22	15	AEF60709	Aef60709 Mouse mic
20	22	100.0	22	15	AEE26704	Aee26704 Hsa miR-1
21	22	100.0	22	15	AEE26638	Aee26638 hsa-miR-1
22	22	100.0	22	15	AEE26636	Aee26636 Mouse mic
23	22	100.0	22	15	AEF25393	Aef25393 Human mRN
24	22	100.0	22	27	ADX03789	Adx03789 Human pri
25	22	100.0	22	30	AEF00087	Aef00087 DNA probe
26	22	100.0	22	40	AEB92912	Aeb92912 Human pri
27	22	100.0	22	70	ADX04205	Adx04205 Mouse pri
28	22	100.0	22	83	ADO17089	Ado17089 Human mic
29	22	100.0	22	83	AEB92620	Aeb92620 Human mic
30	22	100.0	22	83	AED35990	Aed35990 Human miR
31	22	100.0	22	83	AEE26703	Aee26703 Hsa miR-1
32	22	100.0	22	83	AEE99543	Aee99543 Mouse miR
33	22	100.0	22	83	AEE99350	Aee99350 Human mic
34	22	100.0	22	108	AEB92619	Aeb92619 Human pri
35	22	100.0	22	110	ADX03045	Adx03045 Human pri
36	22	100.0	22	110	ADX03080	Adx03080 Human pri
37	22	100.0	22	310	ADX03808	Adx03808 Human gen
38	22	100.0	22	4214	AAK72317	Aak72317 Human imm
39	22	95.5	21	4	ADA00022	Ada00022 D. melano
40	21	95.5	21	14	ADX04045	Adx04045 Human mat
41	21	95.5	21	14	ADX04624	Adx04624 Antisense
42	18.8	85.5	21	7808	ADZ45650	Adz45650 Human pap
43	18.8	85.5	21	7824	ADZ45651	Adz45651 Human pap
44	18	81.8	23	12	ADO17093	Ado17093 Human miR
45	17.8	80.9	21	14	ADX85401	Adx85401 Human/mo

ALIGNMENTS

RESULT 1
ADA00084
ID   ADA00084 standard; RNA; 22 BP.
XX
AC   ADA00084;
XX
DT   06-NOV-2003 (first entry)
XX
DE   Human miRNA sequence miR-15 SEQ ID NO:81.
XX
KW   Drosophila melanogaster; human; mouse; microRNA; miRNA; cytostatic;
KW   gene therapy; diagnostic; therapeutic; developmental modulator;
KW   pathogenic modulator; cancer; B-cell chronic leukaemia;
KW   tissue reprogramming; sn.
XX
OS   Homo sapiens.
XX
PN   WO200302459-A2.
XX
PD   10-APR-2003.
XX
PF   27-SEP-2002; 2002WO-EP010881.
XX
PR   28-SEP-2001; 2001EP-00123453.
PR   22-MAR-2002; 2002EP-00006712.
PR   26-JUL-2002; 2002EP-00016772.
XX
PA   (PLAC) MAX PLANCK GES FOERDERUNG.
XX
PI   Tuschl T, Lagos-Quintana M, Lendeckel W, Meyer J, Rauhut R;
XX
PT   New nucleic acid molecule for diagnostic and therapeutic applications and
PT   as a marker or a modulator of developmental or pathogenic processes, e.g.
PT   cancer, comprises microRNAs of a Drosophila melanogaster, a human or a
PT   mouse.
XX
PS   Claim 1; Page 28; 138pp; English.
XX
CC   The present invention describes an isolated nucleic acid molecule (1)

WPI; 2003-381637/36.

CC comprising a nucleotide sequence of Drosophila melanogaster, human or
CC mouse microRNAs (miRNAs), or their precursors, a complement of it, a
CC nucleotide sequence that has an affinity of at least 80% to them or a
CC nucleotide sequence that hybridises under stringent conditions to them.
CC Also described: (1) a pharmaceutical composition containing the nucleic
CC acid and, optionally, a carrier; and (2) identifying miRNA molecules or
CC precursor molecules, comprising ligating 5'- and 3'-adapter molecules to
CC the ends of a size-fractionated RNA population, reverse transcribing the
CC adapter-containing RNA population and characterising the reverse
CC transcription products. (I) has cytostatic activity, and can be used in
CC gene therapy. The pharmaceutical composition is useful for diagnostic and
CC therapeutic applications, and as a marker or a modulator of developmental
CC or pathogenic processes, particularly of cancer (e.g. B-cell chronic
CC leukaemia) or gene expression. The miRNA molecules may also be used in
CC tissue reprogramming procedures. The present sequence represents an miRNA
CC sequence from the present invention.
XX
SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Qy
        Query Match   100.0%; Score 22; DB 8; Length 22;
        Best Local Similarity   100.0%; Pred. No. 0.35;
        Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
          ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 2
ID ADA00122 standard; RNA; 22 BP.
XX
AC ADA00122;
XX
DT 06-NOV-2003 (first entry)
XX
DE Mouse miRNA sequence miR-15a SEQ ID NO:119.
XX
KW Drosophila melanogaster; human; mouse; microRNA; miRNA; cytostatic;
KW gene therapy; diagnostic; therapeutic; developmental modulator;
KW pathogenic modulator; cancer; B-cell chronic leukaemia;
KW tissue reprogramming; ss.
XX
OS Mus sp.
XX
PN WO200302459-A2.
XX
PD 10-APR-2003.
XX
PF 27-SEP-2002; 2002WO-EP010881.
XX
PR 28-SEP-2001; 2001EP-0012345J.
PR 22-MAR-2002; 2002EP-0005712.
PR 26-JUL-2002; 2002EP-0016772.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG.
XX
PI Tuschl T, Lagos-Quintana M, Lendeckel W, Meyer J, Rauhut R;
XX
DR WPI; 2003-381637/36.
XX
PT New nucleic acid molecule for diagnostic and therapeutic applications and
PT as a marker or a modulator of developmental or pathogenic processes, e.g.
PT cancer, comprises microRNAs of a Drosophila melanogaster, a human or a
PT mouse.
XX
PS Claim 1; Page 31; 138pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a nucleotide sequence of Drosophila melanogaster, human or
CC mouse microRNAs (miRNAs), or their precursors, a complement of it, a
CC nucleotide sequence that has an affinity of at least 80% to them or a
CC nucleotide sequence that hybridises under stringent conditions to them.

CC Also described: (1) a pharmaceutical composition containing the nucleic
CC acid and, optionally, a carrier; and (2) identifying miRNA molecules or
CC precursor molecules, comprising ligating 5'- and 3'-adapter molecules to
CC the ends of a size-fractionated RNA population, reverse transcribing the
CC adapter-containing RNA population and characterising the reverse
CC transcription products. (I) has cytostatic activity, and can be used in
CC gene therapy. The pharmaceutical composition is useful for diagnostic and
CC therapeutic applications, and as a marker or a modulator of developmental
CC or pathogenic processes, particularly of cancer (e.g. B-cell chronic
CC leukaemia) or gene expression. The miRNA molecules may also be used in
CC tissue reprogramming procedures. The present sequence represents an miRNA
CC sequence from the present invention.
XX
SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Qy
        Query Match   100.0%; Score 22; DB 8; Length 22;
        Best Local Similarity   100.0%; Pred. No. 0.35;
        Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db
Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
          ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 3
ID ADO17091 standard; RNA; 22 BP.
XX
AC ADO17091;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human miR15 processed RNA sequence SeqID3.
XX
KW miR15; miR16; cancer; proliferation; cancer cell; cytostatic;
KW gene therapy; chronic lymphocytic leukaemia; prostate cancer; micro RNA;
KW chromosome 13q14; human; ss.
XX
OS Homo sapiens.
XX
PN WO2004043387-A2.
XX
PD 27-MAY-2004.
XX
PF 12-NOV-2003; 2003WO-US035777.
XX
PR 13-NOV-2002; 2002US-0425864P.
PR 09-MAY-2003; 2003US-0469464P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Croce CM, Calin GA;
XX
DR WPI; 2004-400825/37.
XX
PT Treating an miR15 or miR16 mediated cancer, i.e. chronic lymphocytic
PT leukaemia or prostate cancer, comprises administering to the subject an
PT miR15 or miR16 gene product.
XX
PS Claim 64; SEQ ID NO 3; 73pp; English.
XX
CC This invention relates to a novel method of treating an miR15 or miR16
CC mediated cancer in a subject which comprises administering to the subject
CC an amount of an isolated miR15 or miR16 gene product such that
CC proliferation of miR15 or miR16 mediated cancer cells in inhibited. The
CC miR15 and miR16 micro RNA genes are localised to 13q14 in humans, a
CC region that is deleted in a significant portion of subjects suffering
CC from chronic lymphocytic leukaemia or prostate cancer. The products of
CC the miR15 and miR16 genes have also been found to inhibit the neoplastic
CC or tumourigenic growth of chronic lymphocytic leukaemia or prostate
CC cancer cells. The invention may be useful for the production of compounds
CC with a cytostatic activity. In addition the invention may also be useful
CC for gene therapy using the miR15 or miR16 gene product. The methods and

```
CC   compositions are useful in diagnosing and treating miR15 or miR16
CC   mediated cancer, i.e. chronic lymphocytic leukaemia or prostate cancer.
CC   The present sequence is that of the human miR15 processed RNA sequence
CC   which is used in the method of the invention.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 7 U; 0 Other;

     Query Match             100.0%;  Score 22;  DB 12;  Length 22;
     Best Local Similarity   100.0%;  Pred. No. 0.35;
     Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 UAGCAGCACAUAAUGGUUUGUG 22
               |||||||||||||||||||||||
Db           1 UAGCAGCACAUAAUGGUUUGUG 22


RESULT 4
ID   ADP84065      standard; RNA; 22 BP.
XX
AC   ADP84065;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Small nucleotide detection-related human miRNA SeqID62.
XX
KW   small nucleic acid detection; interfering RNA; detection structure;
KW   miRNA; micro RNA; siRNA; short interfering RNA; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO200405701-A2.
XX
PD   08-JUL-2004.
XX
XX
DR   WPI; 2004-500306/47.
XX
PF   18-DEC-2002; 2002US-0434518P.
PR   18-DEC-2002; 2002US-0434518P.
PR   18-DEC-2003; 2003US-00740256.
XX
PA   (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI   Dahlberg JE, Allawi HT, Lyamichev V, Neri BP, Olson-Munoz M,
PI   Chehak L, Olson SM;
XX
PS   Example 2; SEQ ID NO 62; 97pp; English.
XX
PT   Detecting small nucleic acids, such as miRNA and siRNA, by hybridizing an
PT   interfering RNA target to at least one nucleic acid that contains
PT   sequence not complementary to the interfering RNA target to generate a
PT   detection structure.
XX
CC   This invention relates to a novel method of detecting small nucleic acids
CC   which comprises hybridizing an interfering RNA target to at least one
CC   nucleic acid that contains sequence not complementary to the interfering
CC   RNA target to generate a detection structure, and detecting the detection
CC   structure. The present invention is useful for detecting and
CC   characterising interfering RNA such as miRNAs (micro RNAs) and siRNAs
CC   (short interfering RNAs), and quantifying interfering RNA expression. The
CC   present sequence is that of an oligonucleotide which was used in the
CC   exemplification of the invention.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 7 U; 0 Other;

     Query Match             100.0%;  Score 22;  DB 12;  Length 22;
     Best Local Similarity   100.0%;  Pred. No. 0.35;
     Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 UAGCAGCACAUAAUGGUUUGUG 22
               |||||||||||||||||||||||
Db           1 UAGCAGCACAUAAUGGUUUGUG 22
```

```
RESULT 5
ID   ADR83121      standard; RNA; 22 BP.
XX
AC   ADR83121;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Human miRNA oligo that modulates expression of human target mRNA Seq 23.
XX
KW   human; ss; miRNA; microRNA; ontogenesis; cell therapy; cancer;
KW   immune disease; nerve disorder; amyotrophic lateral sclerosis;
KW   Parkinson's disease; Alzheimer's disease; inflammatory disease;
KW   siRNA silencing precursor; cytostatic; immunosuppressive; nootropic;
KW   neuroprotective; antiinflammatory; immunotherapy.
XX
OS   Homo sapiens.
XX
PN   WO200407622-A2.
XX
XX
DR   WPI; 2004-653393/63.
XX
PI   Taira K, Kawasaki H;
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PT   the target gene.
PT   a polynucleotide that forms a duplex region with an mRNA transcribed from
PT   immune disease, or a nerve disorder, comprises introducing into the cell
PT   mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that
XX
PF   10-FEB-2004; 2004WO-JP001433.
PR   10-FEB-2003; 2003US-0445829P.
XX
PS   Claim 6; SEQ ID NO 23; 865pp; English.
XX
CC   Modulating expression of a target gene in a cell, for treating cancer, an
CC   immune disease, or a nerve disorder, comprises introducing into the cell
CC   a polynucleotide that forms a duplex region with an mRNA transcribed from
CC   the target gene.
CC
CC   This invention relates to a novel method for modulating the expression of
CC   a target gene in a cell. Specifically, it refers to the introduction into
CC   a cell of a polynucleotide that forms a duplex region with an mRNA
CC   transcribed from the target gene, where the duplex region comprises a
CC   mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that
CC   regulates mRNA at a post-transcriptional level. The present invention
CC   describes a method for controlling ontogenesis of a mammal, function of a
CC   mammalian cell, differentiation of a mammalian cell or viability of a
CC   mammalian cell in the post-transcriptional phase, which comprises
CC   introducing a plasmid vector comprising a promoter and nucleic acid
CC   molecule expressing an mRNA or siRNA silencing precursor to the miRNA.
CC   Accordingly, it provides a cell therapy method for treating cancer,
CC   immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,
CC   Parkinson's disease, or Alzheimer's disease) or an inflammatory disease
CC   by introducing into the cell the miRNA, siRNA silencing precursor to the
CC   miRNA or the plasmid vector. As such, they can be developed into
CC   pharmaceutical compositions that exhibit cytostatic, immunosuppressive,
CC   nootropic, neuroprotective and antiinflammatory activities and hence can
CC   be used for immunotherapy. This oligonucleotide sequence is a human miRNA
CC   oligo that modulates expression of a target human gene, given in an
CC   exemplification of the invention.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 7 U; 0 Other;

     Query Match             100.0%;  Score 22;  DB 13;  Length 22;
     Best Local Similarity   100.0%;  Pred. No. 0.35;
     Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 UAGCAGCACAUAAUGGUUUGUG 22
               |||||||||||||||||||||||
Db           1 UAGCAGCACAUAAUGGUUUGUG 22
```

```
RESULT 6
XX
ID   ADX03284/c standard; DNA; 22 BP.
XX
AC   ADX03284;
XX
DT   05-MAY-2005 (first entry)
XX
DE   Antisense oligonucleotide targeting a human miRNA, ISIS327951.
XX
KW   Antisense oligonucleotide; ss; RNA interference; gene silencing;
KW   Cytostatic; Antidiabetic; Anorectic; Antilipemic; Antiarteriosclerotic;
KW   Hypotensive; Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW   Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW   angiogenesis disorder; cardiovascular disease;
KW   non-insulin dependent diabetes; endocrine disease;
KW   gastrointestinal disease; metabolic disorder; obesity;
KW   nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
KW   hypertension; anorexia nervosa; nutritional disorder;
KW   psychiatric disorder; Alzheimers disease; degeneration;
KW   neurological disease; nervous system injury; neurodegenerative disease;
KW   neurological disorder; 2'-O-methoxyethyl; 2'MOE; phosphorothioate.
XX
OS   Homo sapiens.
XX
PN   WO2005013901-A2.
XX
PD   17-FEB-2005.
XX
PF   30-JUL-2004; 2004WO-US025300.
XX
PR   31-JUL-2003; 2003US-0492056P.
PR   31-OCT-2003; 2003US-0516303P.
PR   19-DEC-2003; 2003US-0531596P.
PR   14-APR-2004; 2004US-0562417P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF;
PI   Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;
PI   Peralta E;
XX
DR   WPI; 2005-163123/17.
XX
PT   New oligomeric compound that can hybridize with or sterically interfere
PT   with nucleic acid molecules comprising or encoding small non-coding RNA
PT   targets, useful for treating e.g., cancer and diabetes.

PS   Example 5; SEQ ID NO 369; 854pp; English.

CC   The invention relates to an oligomeric compound comprising a first region
CC   and a second region, where at least one region contains a modification,
CC   and a portion of the oligomeric compound is targeted to a small non-
CC   coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC   precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC   comprising a first oligomeric compound and a second oligomeric compound
CC   (where at least one of the oligomeric compounds contains a modification,
CC   at least a portion of the first oligomeric compound is capable of
CC   hybridizing with at least a portion of the second oligomeric compound,
CC   and at least a portion of the first oligomeric compound is targeted to a
CC   small non-coding RNA target nucleic acid), a pharmaceutical composition
CC   comprising the composition cited above (and a carrier), a kit or assay
CC   device comprising the composition, modulating the expression of a small
CC   non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC   treating or preventing a disease or disorder associated with a small non-
CC   coding RNA target nucleic acid, treating a condition in an animal,
CC   treating or preventing a disease or disorder associated with CD36,
CC   methods of screening an oligomeric compound for an effect on miRNA,
CC   methods of screening a miRNA precursor for an effect in miRNA
CC   signaling, methods of modulating translation (or apoptosis, conversion of
CC   a precursor miRNA into miRNA, or cellular differentiation), identifying
CC   an RNA transcript bound to a small non-coding RNA, arresting (or
CC   delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC   segregation, a method of triggering apoptosis, detecting a miRNA
CC   precursor, identifying a miRNA target, modulating cellular
CC   differentiation, treating a condition associated with adipocyte
CC   differentiation in an animal, treating/preventing a disease/disorder
CC   associated with aberrant regulation of the cell cycle by miRNAs,
CC   maintaining a pluripotent stem cell and identifying a small non-coding
CC   RNA binding site. The oligomeric compound is targeted to a region
CC   flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC   increase in expression of a pri-miRNA. The compounds and compositions are
CC   useful for treating a disease or disorder resulting from chromosomal non-
CC   disjunction, altered methylation, acetylation, or pseudouridylation state
CC   of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC   neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC   hyperlipidemia, atherosclerosis, atherogenesis, hypertension, anorexia,
CC   Alzheimer's disease, a central nervous system injury or neurodegenerative
CC   disorder. The present sequence is an antisense oligonucleotide targeting
CC   an miRNA.
XX
SQ   Sequence 22 BP; 7 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match             100.0%;  Score 22;  DB 14;  Length 22;
Best Local Similarity   68.2%;  Pred. No. 0.35;
Matches   15;  Conservative   7;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              ||||||||||||||||::||:|
Db         22 TAGCAGCACATAATGGTTTGTG 1


RESULT 7
ADX03184
XX
ID   ADX03184 standard; RNA; 22 BP.
XX
AC   ADX03184;
XX
DT   05-MAY-2005 (first entry)
XX
DE   Human microRNA (miRNA) mir-15a-1.
XX
KW   MicroRNA; ds; RNA interference; gene silencing; Cytostatic; Antidiabetic;
KW   Anorectic; Antilipemic; Antiarteriosclerotic; Hypotensive;
KW   Neuroprotective; Nootropic; Antiangiogenic; Anabolic;
KW   Eating-Disorders-Gen.; hyperproliferation; cancer; neoplasm;
KW   angiogenesis disorder; cardiovascular disease;
KW   non-insulin dependent diabetes; endocrine disease;
KW   gastrointestinal disease; metabolic disorder; obesity;
KW   nutritional disorder; hyperlipidemia; atherosclerosis; atherogenesis;
KW   hypertension; anorexia nervosa; nutritional disorder;
KW   psychiatric disorder; Alzheimers disease; degeneration;
KW   neurological disease; nervous system injury; neurodegenerative disease;
KW   neurological disorder.
XX
OS   Homo sapiens.
XX
PN   WO2005013901-A2.
XX
PD   17-FEB-2005.
XX
PF   30-JUL-2004; 2004WO-US025300.
XX
PR   31-JUL-2003; 2003US-0492056P.
PR   31-OCT-2003; 2003US-0516303P.
PR   19-DEC-2003; 2003US-0531596P.
PR   14-APR-2004; 2004US-0562417P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Esau C, Lollo B, Bennett CF, Freier SM, Griffey RH, Baker BF;
PI   Vickers T, Marcusson EG, Koller E, Swayze EE, Jain R, Bhat B;
PI   Peralta E;
XX
DR   WPI; 2005-163123/17.
```

```
XX
PT  New oligomeric compound that can hybridize with or sterically interfere
PT  with nucleic acid molecules comprising or encoding small non-coding RNA
PT  targets, useful for treating e.g., cancer and diabetes.
XX
PS
XX
PT  Example 4; SEQ ID NO 269; 854pp; English.
XX

CC  The invention relates to an oligomeric compound comprising a first region
CC  and a second region, where at least one region contains a modification,
CC  and a portion of the oligomeric compound is targeted to a small non-
CC  coding RNA target nucleic acid that is miRNA (micro-RNA), or its
CC  precursor (primary-miRNA, pri-miRNA). Also included are a composition
CC  comprising a first oligomeric compound and a second oligomeric compound
CC  (where at least one of the oligomeric compounds contains a modification,
CC  at least a portion of the first oligomeric compound is capable of
CC  hybridizing with at least a portion of the second oligomeric compound,
CC  and at least a portion of the first oligomeric compound is targeted to a
CC  small non-coding RNA target nucleic acid), a pharmaceutical composition
CC  comprising the composition cited above (and a carrier), a kit or assay
CC  device comprising the composition, modulating the expression of a small
CC  non-coding RNA target nucleic acid in a cell (or tissue or animal),
CC  treating or preventing a disease or disorder associated with a small non-
CC  coding RNA target nucleic acid, treating a condition in an animal,
CC  treating or preventing a disease or disorder associated with CD36,
CC  methods of screening an oligomeric compound for an effect on miRNA
CC  precursor, identifying a miRNA target, modulating cellular
CC  differentiation, treating a condition associated with adipocyte
CC  differentiation, treating/preventing a disease/disorder
CC  signaling, methods of screening a miRNA precursor for an effect in miRNA
CC  signaling, methods of modulating translation (or apoptosis, conversion of
CC  a precursor miRNA into miRNA, or cellular differentiation), identifying
CC  an RNA transcript bound to a small non-coding RNA, arresting (or
CC  delaying) entry of a cell at the G2/M phase, interfering with chromosome
CC  segregation, a method of triggering apoptosis, detecting a miRNA
CC  precursor, identifying a miRNA target, modulating cellular
CC  differentiation, treating a condition associated with adipocyte
CC  differentiation, treating a disease/disorder
CC  associated with aberrant regulation of the cell cycle by miRNAs,
CC  maintaining a pluripotent stem cell and identifying a small non-coding
CC  RNA binding site. The oligomeric compound is targeted to a region
CC  flanking a Drosha cleavage site within a pri-miRNA. It stimulates an
CC  increase in expression of a pri-miRNA. The compounds and compositions are
CC  useful for treating a disease or disorder resulting from chromosomal non-
CC  disjunction, altered methylation, acetylation, or pseudouridylation state
CC  of chromosomes, such as a hyperproliferative condition (e.g. cancer,
CC  neoplasia or angiogenesis), diabetes (Type 2 diabetes), obesity,
CC  hyperlipidemia, atherosclerosis, hypertension, anorexia,
CC  Alzheimer's disease, a central nervous system injury or neurodegenerative
CC  disorder. The present sequence is a mature miRNA of the invention.
XX
SQ  Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
XX
XX

Query Match       100.0%;  Score 22;  DB 14;  Length 22;
Best Local Similarity   100.0%;
Matches 22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db  1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 8
ADY30915
ID   ADY30915 standard; DNA; 22 BP.
XX
AC   ADY30915;
XX
DT   05-MAY-2005 (first entry)
XX
DE   Micro RNA (miRNA)-related DNA targeted to human E2F3/EIF5A2/FOXA1 -SEQ 7.
XX
KW   miRNA; micro RNA; RNA interference; gene silencing;
KW   E2F transcription factor 3; E2F3;
KW   eukaryotic translation initiation factor 5A2; EIF5A2; forkhead box A1;
KW   FOXA1; hepatocyte nuclear factor 3 alpha; HNF3alpha; ss.
XX
```

```
OS   Homo sapiens.
XX
PN   WO2005017145-A1.
XX
PD   24-FEB-2005.
XX
PF   12-AUG-2004; 2004WO-JP011624.
XX
PR   13-AUG-2003; 2003JP-00293129.
XX
PA   (NIBI-) JAPAN BIOLOGICAL INFORMATICS CONSORTIUM.
PA   (BITS-) BITS CO LTD.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PI   Barrero Roberto Antonio, Tamura T, Imanishi T, Gojobori T;
PI   Taira K, Kawasaki H;
XX
DR   WPI; 2005-196094/20.
XX
PS
XX
PT   Identifying a gene under regulation of functional RNA, involves setting
PT   ambiguity of different standards in conserved and unconserved region of
PT   functional RNA, searching for gene which is complementary to functional
PT   RNA.
XX
PS
XX
PT   Claim 8; SEQ ID NO 7; 38pp; Japanese.
XX

CC   The invention relates to a novel method for identifying or presuming a
CC   functional miRNA (micro RNA) molecule of base length of 16-25 and a gene
CC   which is regulated as a result of targeting by the miRNA. The method
CC   comprises determining and classifying the base sequences of functional
CC   RNA molecules into conserved and unconserved regions, setting ambiguities
CC   of different standards in these regions and searching for a candidate
CC   gene which has a base sequence complementary to the functional RNA
CC   molecule. The method of the invention may be useful for identifying a
CC   gene whose expression is under regulation by a functional RNA molecule of
CC   base length of 16-25. The method is thus useful for developing treatments
CC   for a disease or disorder for treating a disease by controlling the biological
CC   function of the target gene. The current sequence is that of a micro RNA
CC   (miRNA)-related DNA of the invention which is targeted to a human gene.
CC   Specifically, human E2F transcription factor 3 (E2F3), eukaryotic
CC   translation initiation factor 5A2 (EIF5A2) and forkhead box A1 (FOXA1,
CC   hepatocyte nuclear factor 3 alpha, HNF3alpha) are referred to in claim 9.
XX
PS
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 7 T; 0 U; 0 Other;
XX
XX

Query Match       100.0%;  Score 22;  DB 14;  Length 22;
Best Local Similarity   100.0%;
Matches 22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db  1 TAGCAGCACATAATGGTTTGTG 22

RESULT 9
ADX85423
ID   ADX85423 standard; RNA; 22 BP.
XX
AC   ADX85423;
XX
DT   05-MAY-2005 (first entry)
XX
DE   Human/mouse miR-15 microRNA that binds hOMP1 target mRNA.
XX
KW   microRNA recognition element; MRE; bioinformatics; gene expression; ss.
XX
OS   Homo sapiens.
OS   Mus sp.
XX
FH   Key        Location/Qualifiers
FT
FT   misc_binding  1..17
FT                 /*tag=  a
FT                 /bound_moiety= "hOMP1 MRE"
```

```
Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      |||||||||:||:||:|::::|
Db  1 TAGCAGCGCATATATGGTTTGTG 22
```

Query Match   68.2%; Score 22; DB 14; Length 22;
Best Local Similarity   ; Conservative   7; Mismatches   0; Indels   0; Gaps   0;
Matches 15;

FT
FT   /note= "Forms double stranded region with nucleotides 17-1"
XX
PN   WO2005017111-A2.
XX
PD   24-FEB-2005.
XX
PF   15-JUL-2004; 2004WO-US022934.
XX
PR   15-JUL-2003; 2003US-0487321P.
XX
PA   (UPEN-) UNIV PENNSYLVANIA.
XX
PI   Hatzigeorgiou AG, Mourelatos 2;
XX
DR   WPI; 2005-182352/19.
XX
PS   Example 1; Fig 6; 51pp; English.
XX
PT   Identifying a microRNA-recognition element by comparing the degree of complementarity of a microRNA nucleotide sequence to an mRNA sequence.
XX
CC   This invention relates to a novel method for identifying a microRNA-recognition element (MRE). Specifically, it refers to comparing the degree of complementarity of a microRNA nucleotide sequence (miRNA) to an mRNA target sequence in order to identify the presence of a sequence that is indicative of an MRE for the microRNA. In particular, it refers to miRNA-MRE recognition rules that allow prediction of human and mouse miRNA targets. The present invention also describes determining the free energy of the microRNA bound to the selected 3' untranslated region of an mRNA sequence i.e. the MRE sequence. Furthermore, it provides an oligonucleotide that is synthesized having the sequence of the generated microRNA and contacting the microRNA with a cell expressing the mRNA in order to down regulate expression of that mRNA. It describes a system for identifying a microRNA-recognition element as comprising an interface for inputting mRNA sequences, a database of mRNA sequences or a link for connecting to a remote data input interface, data or a database of mRNA sequences, and a processor with instructions for comparing mRNA sequences to microRNA sequences to identify an MRE. This oligonucleotide is a human/ mouse microRNA sequence that binds to a microRNA-recognition element of the target mRNA given in an exemplification of the invention.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
XX

Qy   Query Match   100.0%;   Score 22;   DB 14;   Length 22;
Best Local Similarity   100.0%;   Pred. No. 0.35;
Matches 22;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
        ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22
```

RESULT 10

ID   AD220390
AD220390 standard; RNA; 22 BP.
XX
AC   AD220390;
XX
DT   16-JUN-2005   (first entry)
XX
DE   Human hematopoietic miRNA, miR-15a B1_F06-2, SEQ ID NO: 9 #2.
XX
KW   Expression; gene therapy; hematological disease; cancer; infection; cytostatic; antibacterial; virucide; fungicide; antimicrobial; neoplasm; ss; micro RNA; miRNA.
XX
OS   Homo sapiens.
XX
PN   US20050075492-A1.
XX
PD   07-APR-2005.
XX

PF
XX
PR   07-AUG-2003; 2003US-0492339P.
XX
PA   (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Chen C, Bartel D, Lodish H;
XX
DR   WPI; 2005-283812/29.
XX
PT   Disclosure; SEQ ID NO 9; 39pp; English.
XX
CC   New precursor microRNA molecule comprises isolated nucleic acid comprising a stem-loop structure and a microRNA flanking sequence, useful for treating hematopoietic disorders including cancers, viral, bacterial, or fungal infections.
XX
CC   The present invention relates to a precursor microRNA (miRNA) molecule comprising a stem-loop structure and a microRNA flanking sequence. The invention also provides a method for producing miRNA. The invention is useful for treating hematopoietic disorders including cancers, e.g. leukemia, lymphoma, bladder cancer, brain cancer, head and neck cancer, prostate cancer, or rectal cancer and infections. The precursor miRNA is useful for regulating the expression of protein-coding genes at the posttranscriptional level and also be used as therapeutics and as research tools, e.g. analyzing gene function. The invention is useful in gene therapy. The present sequence is the human hematopoietic miRNA which plays a role in hematopoiesis. The current sequence is that of the human miRNA which is located on chromosome 13q13.3. Note: The present sequence is the SEQ ID NO: 9 which is shown on page 7. This sequence differs from the SEQ ID NO: 9 given in the sequence listing (see AD220370).
XX
PS
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
XX

Qy   Query Match   100.0%;   Score 22;   DB 14;   Length 22;
Best Local Similarity   100.0%;   Pred. No. 0.35;
Matches 22;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
        ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22
```

RESULT 11

ID   AEC36205
AEC36205 standard; RNA; 22 BP.
XX
AC   AEC36205;
XX
DT   03-NOV-2005   (first entry)
XX
DE   Nucleotide sequence of known human miRNA #9.
XX
KW   RNA interference; gene silencing; microRNA; miRNA; gene therapy; Huntingtons chorea; cardiovascular disease; cardiovascular-gen.; immune disorder; immunomodulator; liver disease; hepatotropic; gastrointestinal disease; viral infection; virucide; infection; pain; analgesic; neurological disease; metabolic disorder; metabolic; metabolic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200507809096-A2.
XX
PD   25-AUG-2005.
XX
PF   09-FEB-2005; 2005WO-US004206.
XX
PR   09-FEB-2004; 2004US-0543467P.
XX
PA   (UYMA-) UNIV MASSACHUSETTS.
XX

RESULT 12

```
ID   AED35921 standard; DNA; 22 BP.
XX
AC   AED35921;
XX
DT   15-DEC-2005 (first entry)
XX
DE   Hsa-miR-15a DNA target.
XX
KW   RNA interference; RNA purification; RNA amplification; gene silencing;
KW   RNA detection; micro RNA; miRNA; miR-15a; ss.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   modified_base  22
FT                  /*tag= a
FT                  /mod_base= OTHER
FT                  /note= "OTHER= 3' Phosphorylated"
XX
PN   WO200509029-A2.
XX
PD   20-OCT-2005.
XX
PF   07-APR-2005; 2005WO-DK000239.
XX
PR   07-APR-2004; 2004DK-00000578.
PR   23-JUL-2004; 2004DK-0001146.
PR   11-AUG-2004; 2004DK-0001218.
PR   15-OCT-2004; 2004DK-0001587.
PR   28-JAN-2005; 2005DK-0000140.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Nielsen PS, Norholm M;
PI   Jacobsen N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;
XX
DR   WPI; 2005-714540/73.
XX
PT   Isolating, purifying, amplifying, detecting, identifying, quantifying or
XX
PI   Zamore PD, Aronin N, Broderick J;
XX
DR   WPI; 2005-571602/58.
XX
PT   New RNA-silencing agent comprising an mRNA targeting moiety, a linking
PT   moiety, and a miRNA recruiting moiety, useful for repressing translation
PT   of a target mRNA for treating Huntington's disease.
XX
PS   Disclosure; Page 11; 80pp; English.
XX
CC   The specification describes a RNA-silencing agent, comprising an mRNA
CC   targeting moiety, a linking moiety, and a microRNA (miRNA) recruiting
CC   moiety. The RNA-silencing agent of the invention is useful for the
CC   manufacture of medicament for repressing mutant gene expression, such as
CC   repressing translation of a target mRNA. It is useful for treating
CC   Huntington's disease in this manner. The agent may also be useful in the
CC   treatment of one or more of cellular proliferative and/or differentiative
CC   disorders, cardiovascular disorders, immune disorders, hematopoietic
CC   disorders, liver disorders, viral diseases, pain or metabolic disorders.
CC   AEC36197-AEC36300 represent known human miRNAs.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Query Match             100.0%;  Score 22;  DB 14;  Length 22;
Best Local Similarity   100.0%;  Pred. No. 0.35;
Matches  22;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              ||||||||||||||||||||||
Db          1 UAGCAGCACAUAAUGGUUUGUG 22
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RESULT 13

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ID   AED35925 standard; RNA; 22 BP.
XX
AC   AED35925;
XX
DT   15-DEC-2005 (first entry)
XX
DE   Hsa-miR-15a RNA target.
XX
KW   RNA interference; RNA purification; RNA amplification; gene silencing;
KW   RNA detection; micro RNA; miRNA; miR-15a; ss.
XX
OS   Homo sapiens.
XX
PN   WO200509029-A2.
XX
PD   20-OCT-2005.
XX
PF   07-APR-2005; 2005WO-DK000239.
XX
PR   07-APR-2004; 2004DK-00000578.
XX
PT   capturing non-coding RNAs such as micro RNA or small interfering RNA
PT   (siRNA), involves using oligonucleotide containing nucleoside analogs.
XX
PS   Example; Page 69; 180pp; English.
XX
CC   The present invention relates to the use of an oligonucleotide for the
CC   isolation, purification, amplification, detection, identification,
CC   quantification or capture of microRNA (miRNA) or small interfering RNA
CC   (siRNA), where the oligonucleotide contains a number of nucleoside
CC   analogs. The method uses 2 anchored target tagging probes, each designed in
CC   combination to detect a complementary target sequence, e.g. a short RNA
CC   sequence, where the first tagging probe hybridizes to a first region
CC   within a target sequence and the second tagging probe hybridizes to a
CC   second region within the same complementary target sequence, e.g. a short
CC   RNA target sequence that is adjacent to the first region. In a preferred
CC   mode, one of the tagging probes is 5' phosphorylated to enable covalent
CC   coupling of the 2 contiguous tagging probes hybridized to the
CC   complementary target sequence by a ligase to form a single
CC   oligonucleotide sequence. The method takes advantage of substitution of
CC   the recognition sequences with high-affinity nucleotide analogs, e.g.
CC   locked nucleic acid (LNA), for sensitive and specific hybridization to
CC   short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is
CC   followed by real-time quantitative PCR (qPCR) of the target sequence,
CC   e.g. ribonucleic acid-templated, covalently joined oligonucleotide
CC   molecules using anchor sequences attached to the tagging probes as
CC   priming sites for the PCR primers and a short detection probe with
CC   sufficient duplex stability to allow binding to the amplicon, and
CC   employing any of a variety of detection principles used in homogeneous
CC   assays. In the preferred mode, the detection probe is substituted with
CC   duplex-stabilizing, high-affinity nucleotide analogs, e.g. LNA, and
CC   preferably oxy-LNA, to allow the use of short detection probes in the
CC   real-time qPCR. The method is useful for detecting and quantifying
CC   individual small RNA molecules in complex mixtures of different nucleic
CC   acids, and for detecting, testing, diagnosing or quantifying miRNAs,
CC   siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA
CC   splice variants implicated in, or connected to, human disease in complex
CC   nucleic acid samples, e.g. from cancer patients. The present sequence is
CC   that of hsa-miR-15a DNA, which was used as a target sequence in a real-
CC   time qPCR assay of human miR-15a in an example from the invention.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 7 T; 0 U; 0 Other;

Query Match             100.0%;  Score 22;  DB 14;  Length 22;
Best Local Similarity   68.2%;  Pred. No. 0.35;
Matches  15;  Conservative  7;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :|||||||||:||:||:::::|
Db          1 TAGCAGCACATAATGGTTTGTG 22
```

PR 23-JUL-2004; 2004DK-00001146.
PR 11-AUG-2004; 2004DK-00001218.
PI
PR 15-OCT-2004; 2004DK-00001587.
PR 28-JAN-2005; 2005DK-00000140.
XX
PA
XX
PR
PR
XX
XX
PN (EXIQ-) EXIQON AS.
XX
PI Jacobsen N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;
PI Nielsen PS, Norholm M;
XX
DR WPI; 2005-714540/73.
XX
PT Isolating, purifying, amplifying, detecting, identifying, quantifying or
PT capturing non-coding RNAs such as micro RNA or small interfering RNA
PT (siRNA), involves using oligonucleotide containing nucleoside analogs.
XX
PS Example; Page 69; 180pp; English.
XX

CC The present invention relates to the use of an oligonucleotide for the
CC isolation, purification, amplification, detection, identification,
CC quantification or capture of microRNA (miRNA) or small interfering RNA
CC (siRNA), where the oligonucleotide contains a number of nucleoside
CC analogs. The method uses 2 anchored tagging probes, each designed in
CC combination to detect a complementary target sequence, e.g. a short RNA
CC sequence, where the first tagging probe hybridizes to a first region
CC within a target sequence and the second tagging probe hybridizes to a
CC second region within the same complementary target sequence, e.g. a short
CC RNA target sequence that is adjacent to the first region. In a preferred
CC mode, one of the tagging probes is 5', phosphorylated to enable covalent
CC coupling of the 2 contiguous tagging probes hybridized to the
CC complementary target sequence by a ligase to form a single
CC oligonucleotide sequence. The method takes advantage of substitution of
CC the recognition sequences with high-affinity nucleotide analogs, e.g.
CC locked nucleic acid (LNA), for sensitive and specific hybridization to
CC short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is
CC followed by real-time quantitative PCR (qPCR) of the target sequence,
CC e.g. ribonucleic acid-templated, covalently joined oligonucleotide
CC sequence, where the first tagging probe hybridizes to a first region
CC priming sites for the PCR primers and a short detection probe with
CC molecules using anchor sequences attached to the tagging probes as
CC sufficient duplex stability to allow binding to the amplicon, and
CC employing any of a variety of detection principles used in homogeneous
CC assays. In the preferred mode, the detection probe is substituted with
CC real-time qPCR. The method is useful for detecting and quantifying
CC individual small RNA molecules in complex mixtures of different nucleic
CC acids, and for detecting, testing, diagnosing or quantifying miRNAs,
CC siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA
CC nucleic acid samples, e.g. from cancer patients. The present sequence is
CC splice variants implicated in, or connected to, human disease in complex
CC that of hsa-miR-15a RNA, which was used as a target sequence in a real-
CC time qPCR assay of human miR-15a in an example from the invention.
XX
SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Qy Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUUGUG 22
||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUGUG 22

RESULT 14
ID AED35991 standard; RNA; 22 BP.
XX
AC AED35991;
XX
DT 15-DEC-2005 (first entry)
XX
DE Human micro RNA miR-15a.

XX
KW RNA interference; RNA purification; RNA amplification; gene silencing;
KW RNA detection; micro RNA; miRNA; miR-15a; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200509029-A2.
XX
PD 20-OCT-2005.
XX
XX
PA (EXIQ-) EXIQON AS.
XX
PI Jacobsen N, Kongsbak L, Kauppinen S, Echwald SM, Mouritzen P;
PI Nielsen PS, Norholm M;
XX
PF 07-APR-2005; 2005WO-DK000239.
XX
DR WPI; 2005-714540/73.
XX
PR 07-APR-2004; 2004DK-00000578.
PR 23-JUL-2004; 2004DK-00001146.
PR 11-AUG-2004; 2004DK-00001218.
PR 15-OCT-2004; 2004DK-00001587.
PR 28-JAN-2005; 2005DK-00000140.
XX
PT Isolating, purifying, amplifying, detecting, identifying, quantifying or
PT capturing non-coding RNAs such as micro RNA or small interfering RNA
PT (siRNA), involves using oligonucleotide containing nucleoside analogs.
XX
PS Disclosure; Fig 29; 180pp; English.
XX

CC The present invention relates to the use of an oligonucleotide for the
CC isolation, purification, amplification, detection, identification,
CC quantification or capture of microRNA (miRNA) or small interfering RNA
CC (siRNA), where the oligonucleotide contains a number of nucleoside
CC analogs. The method uses 2 anchored tagging probes, each designed in
CC combination to detect a complementary target sequence, e.g. a short RNA
CC sequence, where the first tagging probe hybridizes to a first region
CC within a target sequence and the second tagging probe hybridizes to a
CC second region within the same complementary target sequence, e.g. a short
CC RNA target sequence that is adjacent to the first region. In a preferred
CC mode, one of the tagging probes is 5', phosphorylated to enable covalent
CC coupling of the 2 contiguous tagging probes hybridized to the
CC complementary target sequence by a ligase to form a single
CC oligonucleotide sequence. The method takes advantage of substitution of
CC the recognition sequences with high-affinity nucleotide analogs, e.g.
CC locked nucleic acid (LNA), for sensitive and specific hybridization to
CC short target sequences, e.g. miRNAs or siRNAs. The ligation reaction is
CC followed by real-time quantitative PCR (qPCR) of the target sequence,
CC e.g. ribonucleic acid-templated, covalently joined oligonucleotide
CC sequence, where the first tagging probe hybridizes to a first region
CC priming sites for the PCR primers and a short detection probe with
CC molecules using anchor sequences attached to the tagging probes as
CC sufficient duplex stability to allow binding to the amplicon, and
CC employing any of a variety of detection principles used in homogeneous
CC assays. In the preferred mode, the detection probe is substituted with
CC real-time qPCR. The method is useful for detecting and quantifying
CC individual small RNA molecules in complex mixtures of different nucleic
CC acids, and for detecting, testing, diagnosing or quantifying miRNAs,
CC siRNAs, other non-coding RNAs, RNA-edited transcripts or alternative mRNA
CC nucleic acid samples, e.g. from cancer patients. The present sequence is
CC splice variants implicated in, or connected to, human disease in complex
CC that of human miRNA Hsa miR-15a, which was used as the target in examples
CC from the invention.
XX
SQ Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

Qy Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAGCAGCACAUAAUGGUUGUG 22

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Db          1 UAGCAGCACAUAAUGGUUUGUG 22
              |||||||||||||||||||||||
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RESULT 15

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ID   AEDS3385 standard; RNA; 22 BP.
XX
AC   AEDS3385;
XX
DT   29-DEC-2005  (first entry)
XX
DE   Human target / micro RNA oligo, hsa-mir-15.
XX
KW   RNA interference; micro RNA; miRNA; transcription; gene regulation;
KW   microarray; ss.
XX
OS   Homo sapiens.
XX
PN   JP2005296014-A.
XX
PD   27-OCT-2005.
XX
PF   06-APR-2005; 2005JP-0010991S.
XX
PR   06-APR-2004; 2004US-00818956.
XX
PA   (EPPE-) EPPENDORF ARRAY TECHNOLOGIES SA.
XX
PI   Van Veffer C, Lemacre J, Bulov S, Samatheo N;
XX
DR   WPI; 2005-753146/77.
XX
PT   Determining RNA interference mediated transcriptional regulation of cell,
PT   by ligating micro RNA of cell to polynucleotide by which target was
PT   labeled and hybridizing it to probe for transcription material, in array,
PT   detecting signal.
XX
PS   Claim 31; Page 20; 30pp; Japanese.
XX
CC   The invention relates to a novel method for determining RNA interference
CC   (RNAi) mediated transcriptional regulation of a cell, by determining
CC   patterns of at least 3 micro RNAs (miRNAs). The method involves preparing
CC   an array with a capture probe of transcription material from the DNA of a
CC   cell, isolating an miRNA pool existing latently from the cell, extending
CC   the miRNA or ligating it to a polynucleotide with a labeled target,
CC   hybridizing the polynucleotide with a probe in an array and detecting a
CC   signal from the array. The invention further includes a kit for carrying
CC   out the above method. The method is useful for determining RNAi mediated
CC   transcriptional regulation of a cell. This sequence represents a human
CC   target / miRNA oligo for use in a microarray of the invention.
XX
SQ   Sequence 22 BP; 6 A; 3 C; 6 G; 0 T; 7 U; 0 Other;

     UAGCAGCACAUAAUGGUUUGUG                                              22
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Query Match   100.0%;   Score 22; DB 14; Length 22;
Best Local Similarity   100.0%;   Pred. No. 0.35;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy           1 UAGCAGCACAUAAUGGUUUGUG 22
               ||||||||||||||||||||||
Db           1 UAGCAGCACAUAAUGGUUUGUG 22
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
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Run on: November 1, 2006, 20:59:58 ; Search time 38.1333 Seconds
(without alignments)
1079.486 Million cell updates/sec

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Perfect score: 22
Sequence: 1 uagcagcacauaaugguuguug 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17.2	78.2	601	3	US-09-949-016-76948	Sequence 76948, A
	2	17.2	78.2	117807	3	US-09-949-016-15525	Sequence 15525, A
	3	17.2	78.2	189560	3	US-09-949-016-17202	Sequence 17202, A
c	4	17.2	78.2	236341	3	US-09-949-016-13978	Sequence 13978, A
	5	16.8	76.4	601	3	US-09-949-016-110759	Sequence 110759,
	6	16.8	76.4	601	3	US-09-949-016-110920	Sequence 110920,
	7	16.8	76.4	601	3	US-09-949-016-111081	Sequence 111081,
	8	16.8	76.4	601	3	US-09-949-016-111242	Sequence 111242,
	9	16.8	76.4	966	3	US-09-248-796A-5921	Sequence 5921, Ap
c	10	16.8	76.4	2319	3	US-09-070-356-1	Sequence 1, Appli
c	11	16.8	76.4	2334	3	US-08-406-070-1	Sequence 1, Appli
c	12	16.8	76.4	43991	5	US-09-984-429-252	Sequence 252, App
	13	16.8	76.4	174170	3	US-09-949-016-14810	Sequence 14810, A
	14	16.8	76.4	174170	3	US-09-949-016-14811	Sequence 14811, A
	15	16.8	76.4	174318	3	US-09-949-016-11880	Sequence 11880, A
	16	16.8	76.4	174318	3	US-09-949-016-14812	Sequence 14812, A
	17	16.8	76.4	174318	3	US-09-949-016-14813	Sequence 14813, A
	18	16.8	76.4	174318	3	US-09-949-016-17630	Sequence 17630, A
	19	16.6	75.5	601	3	US-09-949-016-36194	Sequence 36194, A
	20	16.6	75.5	601	3	US-09-949-016-54602	Sequence 54602, A
	21	16.6	75.5	601	3	US-09-949-016-54634	Sequence 54634, A
	22	16.6	75.5	601	3	US-09-949-016-54666	Sequence 54666, A
	23	16.6	75.5	601	3	US-09-949-016-119031	Sequence 119031,
	24	16.6	75.5	601	3	US-09-949-016-119067	Sequence 119067,
	25	16.6	75.5	601	3	US-09-949-016-119103	Sequence 119103, A
	26	16.6	75.5	601	3	US-09-949-016-119139	Sequence 119139,
	27	16.6	75.5	601	3	US-09-949-016-119175	Sequence 119175,
	28	16.6	75.5	601	3	US-09-949-016-119211	Sequence 119211,
	29	16.4	74.5	1365	3	US-09-949-016-2063	Sequence 2063, Ap
	30	16.4	74.5	6946	3	US-09-949-016-13805	Sequence 13805, A
	31	16.2	73.6	601	3	US-09-949-016-46039	Sequence 46039, A
c	32	16.2	73.6	601	3	US-09-949-016-92412	Sequence 92412, A
c	33	16.2	73.6	601	3	US-09-949-016-137903	Sequence 137903,
c	34	16.2	73.6	777	3	US-08-956-171E-1156	Sequence 1156, Ap
c	35	16.2	73.6	1140	3	US-08-781-986A-4772	Sequence 4772, Ap
c	36	16.2	73.6	1671	3	US-09-248-796A-4660	Sequence 4660, Ap
c	37	16.2	73.6	4880	10	US-05-175383	Patent No. 5,175383
	38	16.2	73.6	7868	3	US-09-676-519-19	Sequence 19, Appl
	39	16.2	73.6	43576	3	US-09-949-016-12224	Sequence 12224, A
	40	16.2	73.6	52711	3	US-09-949-016-15618	Sequence 15618, A
	41	16.2	73.6	52865	3	US-09-949-016-16267	Sequence 16267, A
c	42	16.2	73.6	54531	3	US-09-949-016-14385	Sequence 14385, A
c	43	16.2	73.6	54602	3	US-09-949-016-13058	Sequence 13058, A
	44	16.2	73.6	72602	3	US-09-949-016-14385	Sequence 14385, A
	45	16.2	73.6	103712	3	US-09-949-016-13058	Sequence 13058, A

ALIGNMENTS

RESULT 1
US-09-949-016-76948
; Sequence 76948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76948
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-76948

Query Match 78.2%; Score 17.2; DB 3; Length 601;
Best Local Similarity 59.1%; Pred. No. 72;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy   1 UAGCAGCACAUAAUGGUUGUUG 22
            || ||||| |||| ||:|||:|
Db   169 TAGAGGCCACAAAAUGGTTTGTG 190

RESULT 2
US-09-949-016-15525
; Sequence 15525, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 15525
; LENGTH: 117807
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15525

Qy   1 UAGCAGGCACAUAAUGGUUUGUG 22
              |||||::|:||:||::||:::|:|
Db   29126 TAGCTGCACATAATGGTCTGTG 29147

Query Match   78.2%; Score 17.2; DB 3; Length 117807;
Best Local Similarity   59.1%; Pred. No. 1.5e+02;
Matches   13; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

US-09-949-016-15525

RESULT 3
US-09-949-016-17202
; Sequence 17202, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 17202
; LENGTH: 189560
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(189560)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17202

Qy   1 UAGCTGACAUAAUGGUUUGUG 22
              ::||||::||:||::|:::|:|
Db   130962 TAGCTGACATAATGGTGTGTG 130983

Query Match   78.2%; Score 17.2; DB 3; Length 189560;
Best Local Similarity   59.1%; Pred. No. 1.6e+02;
Matches   13; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

US-09-949-016-17202

RESULT 4
US-09-949-016-13978
; Sequence 13978, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
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;
; SEQ ID NO 13978
; LENGTH: 236341
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(236341)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13978

Qy   1 UAGCAGGCACAUAAUGGUUUGUG 22
              ||||||||||||||||:||:||:|
Db   187064 TAGCAGGCACAAAAATGGTTTGTG 187043

Query Match   78.2%; Score 17.2; DB 3; Length 236341;
Best Local Similarity   59.1%; Pred. No. 1.7e+02;
Matches   13; Conservative   6; Mismatches   3; Indels   0; Gaps   0;

US-09-949-016-13978

RESULT 5
US-09-949-016-110759
; Sequence 110759, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 110759
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110759

Qy   1 UAGCAGGCACAUAAUGGUUUG 20
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Db   398 TAGCAGGCACATAATGCTATG 417

Query Match   76.4%; Score 16.8; DB 3; Length 601;
Best Local Similarity   65.0%; Pred. No. 1.1e+02;
Matches   13; Conservative   5; Mismatches   2; Indels   0; Gaps   0;

US-09-949-016-110759

RESULT 6
US-09-949-016-110920
; Sequence 110920, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768

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;        PRIOR FILING DATE: 2000-10-03
;        PRIOR APPLICATION NUMBER: 60/231,498
;        PRIOR FILING DATE: 2000-09-08
;        NUMBER OF SEQ ID NOS: 207012
;        SOFTWARE: FastSEQ for Windows Version 4.0
;      SEQ ID NO 110920
;        LENGTH: 601
;        TYPE: DNA
;        ORGANISM: Human
US-09-949-016-110920

Qy        1 UAGCAGCACAUAAUGGUUUG 20
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Db      398 TAGCAGCACATAATGCTATG 417

Query Match           76.4%;     Score 16.8;  DB 3;  Length 601;
Best Local Similarity 65.0%;     Pred. No. 1.1e+02;
Matches   13; Conservative 5; Mismatches  2; Indels  0; Gaps  0;


RESULT 7
US-09-949-016-111081
Sequence 111081, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 111081
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-111081


RESULT 8
US-09-949-016-111242
Sequence 111242, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
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;      SEQ ID NO 111242
;        LENGTH: 601
;        TYPE: DNA
;        ORGANISM: Human
US-09-949-016-111242

Qy        1 UAGCAGCACAUAAUGGUUUG 20
            |||||||||||||||:|::|:|
Db      398 TAGCAGCACATAATGCTATG 417

Query Match           76.4%;     Score 16.8;  DB 3;  Length 601;
Best Local Similarity 65.0%;     Pred. No. 1.1e+02;
Matches   13; Conservative 5; Mismatches  2; Indels  0; Gaps  0;


RESULT 9
US-09-248-796A-5921/c
Sequence 5921, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196,132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE: 1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
;  SEQ ID NO 5921
;    LENGTH: 966
;    TYPE: DNA
;    ORGANISM: Candida albicans
US-09-248-796A-5921

Qy        1 UAGCAGCACAUAAUGGUUUG 20
            |||||||||||||||:|::|:|
Db      398 TAGCAGCACATAATGCTATG 417

Query Match           76.4%;     Score 16.8;  DB 3;  Length 966;
Best Local Similarity 65.0%;     Pred. No. 1.2e+02;
Matches   12; Conservative 6; Mismatches  2; Indels  0; Gaps  0;


RESULT 10
US-09-070-356-1/c
Sequence 1, Application US/09070356
Patent No. 6228631
GENERAL INFORMATION:
;  APPLICANT: Alex Zhu
;  APPLICANT: Jack Goldstein
;  TITLE OF INVENTION: Recombinant a-N-
;  TITLE OF INVENTION: Acetylgalactosaminidase
;  TITLE OF INVENTION: Enzyme and cDNA Encoding
;  TITLE OF INVENTION: Said Enzyme
;  NUMBER OF SEQUENCES: 7
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Amster, Rothstein & Ebenstein
;  STREET: 90 Park Avenue
;  CITY: New York
;  STATE: New York
;  COUNTRY: U.S.A.
;  ZIP: 10016
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
;  COMPUTER: IBM PC Compatible
;  OPERATING SYSTEM: MS-DOS
;  SOFTWARE: Word Processor (ASCII)
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/070,356
;  FILING DATE:
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Qy        3 GCAGCACAUAAUGGUUUGUG 22
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Db      734 GCAGCAAATAATTGTTTGTG 715
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,248
; FILING DATE: March 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REFERENCE/DOCKET NUMBER: 63475/12
; REGISTRATION NUMBER: 34,894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2319
; MOLECULE TYPE:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: chicken liver
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE: library
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY: chicken liver a-N-
; NAME/KEY: acetylgalactosaminidase
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-09-070-356-1

Query Match   76.4%; Score 16.8; DB 3; Length 2319;
Best Local Similarity   60.0%; Pred. No. 1.4e+02;
Matches   12; Conservative   6; Mismatches   2; Indels   0; Gaps   0;

Qy   3 GCAGCACAUAAUGGUUUGUG 22
          |||||||||||::|||::||:|
Db   673 GCAGCACATCCTGGTTTGTG 654

RESULT 11
US-08-406-070-1/c
; Sequence 1, Application US/08406070
; Patent No. 5610063
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel S.
; APPLICANT: Walker, John C.

; TITLE OF INVENTION: A cDNA For
; TITLE OF INVENTION: alpha-N-acetyl-galactosaminidase From Gallus domesticus
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,070
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: UMO P-317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2334 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2316..2334
US-08-406-070-1

Query Match   76.4%; Score 16.8; DB 2; Length 2334;
Best Local Similarity   60.0%; Pred. No. 1.4e+02;
Matches   12; Conservative   6; Mismatches   2; Indels   0; Gaps   0;

Qy   3 GCAGCACAUAAUGGUUUGUG 22
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Db   670 GCAGCACATCCTGGTTTGTG 651

RESULT 12
US-09-984-429-252
; Sequence 252, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P201BP2
; CURRENT APPLICATION NUMBER: US/09/984,429
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/244,591
; PRIOR FILING DATE: 1998-10-08
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/288,143
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US98/21142
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/061,529
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,463
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/071,498
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,527
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/061,536
; PRIOR FILING DATE: 1997-10-09

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;   PRIOR APPLICATION NUMBER: 60/061,532
;   PRIOR FILING DATE: 1997-10-09
;   NUMBER OF SEQ ID NOS: 727
;   SOFTWARE: PatentIn Ver. 2.0
;
;   SEQ ID NO 252
;   LENGTH: 43991
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-984-429-252

Query Match     76.4%;  Score 16.8;  DB 5;  Length 43991;
Best Local Similarity   65.0%;  Pred. No. 2.1e+02;
Matches   13;  Conservative   5;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 UAGCAGCACAUAAUGGUUUG 20
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Db  10240 TAGCAGAACACAAATGGTTTG 10259

RESULT 13
US-09-949-016-14810
;   Patent No. 6812339
;   GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 14810
;   LENGTH: 174170
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174170)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14810

Query Match     76.4%;  Score 16.8;  DB 3;  Length 174170;
Best Local Similarity   65.0%;  Pred. No. 2.5e+02;
Matches   13;  Conservative   5;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 UAGCAGCACAUAAUGGUUUG 20
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Db  56372 TAGCAGCACATAATGGTTTG 56391

RESULT 14
Sequence 14811, Application US/09949016
;   Patent No. 6812339
;   GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
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;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 14811
;   LENGTH: 174170
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174170)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14811

Query Match     76.4%;  Score 16.8;  DB 3;  Length 174170;
Best Local Similarity   65.0%;  Pred. No. 2.5e+02;
Matches   13;  Conservative   5;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 UAGCAGCACAUAAUGGUUUG 20
          :||||||||||:|:||||:|:|
Db  56372 TAGCAGCACATAAATGCTATG 56391

RESULT 15
US-09-949-016-11880
;   Sequence 11880, Application US/09949016
;   Patent No. 6812339
;   GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 11880
;   LENGTH: 174318
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(174318)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11880

Query Match     76.4%;  Score 16.8;  DB 3;  Length 174318;
Best Local Similarity   65.0%;  Pred. No. 2.5e+02;
Matches   13;  Conservative   5;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      1 UAGCAGCACAUAAUGGUUUG 20
          :||||||||||:|:||||:|:|
Db  56520 TAGCAGCACATAAATGCTATG 56539

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GenCore version 5.1.9
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Title: US-10-706-798-3
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Maximum Match 100%
Listing first 45 summaries

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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	22	8	US-10-706-798-3	Sequence 3, Appli
	2	22	100.0	22	10	US-10-490-955-81	Sequence 81, Appl
	3	22	100.0	22	10	US-10-490-955-119	Sequence 119, App
c	4	22	100.0	22	10	US-10-490-955-448	Sequence 448, App
	5	22	100.0	22	10	US-10-740-256A-62	Sequence 62, Appl
c	6	22	100.0	22	10	US-10-909-125-269	Sequence 269, App
c	7	22	100.0	22	10	US-10-909-125-369	Sequence 369, App
	8	22	100.0	22	11	US-10-881-362B-7	Sequence 7, Appli
c	9	22	100.0	22	10	US-11-055-035-16	Sequence 16, Appl
	10	22	100.0	22	10	US-11-102-453-15	Sequence 15, Appl
	11	22	100.0	22	10	US-11-102-453-111	Sequence 111, App
c	12	22	100.0	22	10	US-11-100-897-5	Sequence 5, Appl
	13	22	100.0	22	15	US-11-100-897-73	Sequence 73, Appl
	14	22	100.0	22	15	US-11-171-175-131	Sequence 131, App
c	15	22	100.0	27	16	US-10-909-125-887	Sequence 887, App
	16	22	100.0	22	10	US-10-909-125-1316	Sequence 1316, Ap
	17	22	100.0	70	10	US-10-909-125-1316	Sequence 1316, Ap
	18	22	100.0	8		US-10-706-798-1	Sequence 1, Appli
	19	22	100.0	83		US-10-490-955-248	Sequence 248, App
	20	22	100.0	83		US-10-490-955-305	Sequence 305, App
	21	22	100.0	15		US-11-100-897-72	Sequence 72, Appl
	21	22	100.0	16		US-11-230-992-1	Sequence 1, Appli
	22	22	100.0	83		US-10-909-125-128	Sequence 128, App
	23	22	100.0	110		US-10-909-125-165	Sequence 165, App
	24	22	100.0	110		US-10-909-125-906	Sequence 906, App
	25	22	100.0	310		US-10-490-955-19	Sequence 19, Appl
	26	21	95.5	10		US-10-909-125-1151	Sequence 1151, App
c	27	21	95.5	10		US-10-708-204-1768	Sequence 1768, App
	27	21	95.5	21		US-10-909-125-23	Sequence 23, Appl
	28	21	95.5	21		US-10-708-204-6557	Sequence 6557, Ap
c	29	20	90.9	74		US-10-708-204-6769	Sequence 6769, Ap
	30	20	90.9	76		US-10-972-079-77545	Sequence 77545, A
	31	20	90.9	22		US-10-706-798-5	Sequence 5, Appli
	32	18.8	85.5	23		US-10-909-125-1115	Sequence 1115, App
c	33	18	81.8	600		US-10-909-125-1886	Sequence 1886, Ap
	34	17.4	79.1	21		US-10-490-955-120	Sequence 120, App
	35	17.4	79.1	22		US-10-490-955-449	Sequence 449, App
c	36	17.4	79.1	22		US-10-909-125-246	Sequence 246, App
	37	17.4	79.1	22		US-10-909-125-345	Sequence 345, App
	38	17.4	79.1	22		US-11-171-175-112	Sequence 112, App
	39	17.4	79.1	22		US-11-102-453-112	Sequence 112, App
c	40	17.4	79.1	22		US-11-102-453-132	Sequence 132, App
c	41	17.4	79.1	22		US-11-055-035-206	Sequence 206, App
	42	17.4	79.1	16		US-10-490-955-1286	Sequence 1286, Ap
	43	17.4	79.1	85		US-11-171-175-306	Sequence 306, App
c	44	17.4	79.1	98		US-11-230-992-2	Sequence 2, Appli
	45	17.4	79.1	110		US-10-909-125-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-10-706-798-3
Sequence 3, Application US/10706798
; Publication No. US20040152112A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Calin, George A.
; TITLE OF INVENTION: Compositions and Methods for Cancer
; TITLE OF INVENTION: Diagnosis and Therapy
; FILE REFERENCE: 08321-0126US1
; CURRENT APPLICATION NUMBER: US/10/706,798
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,864
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/469,464
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-706-798-3

Query Match 100.0%; Score 22; DB 8; Length 22;
Best Local Similarity 100.0%;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
        ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22
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RESULT 2
US-10-490-955-81
Sequence 81, Application US/10490955
; Publication No. US20050059005A1
; GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lagos-Quintana, Mariana

; APPLICANT: Lendeckel, Winfried
; APPLICANT: Meyer, Jutta
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 81
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-490-955-81

Query Match   100.0%; Score 22; DB 10; Length 22;
Best Local Similarity   100.0%; Pred. No. 1.9;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
       ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 3
US-10-490-955-119
; Sequence 119, Application US/10490955
; Publication No. US20050059005A1
; GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lagos-Quintana, Mariana
; APPLICANT: Meyer, Jutta
; APPLICANT: Lendeckel, Winfried
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 119
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-490-955-119

Query Match   100.0%; Score 22; DB 10; Length 22;
Best Local Similarity   100.0%; Pred. No. 1.9;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
       ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 4
US-10-490-955-448
; Sequence 448, Application US/10490955
; Publication No. US20050059005A1
; GENERAL INFORMATION:
; APPLICANT: Tuschl, Thomas
; APPLICANT: Lagos-Quintana, Mariana
; APPLICANT: Meyer, Jutta
; APPLICANT: Lendeckel, Winfried
; APPLICANT: Rauhut, Reinhard
; TITLE OF INVENTION: MicroRNA Molecules
; FILE REFERENCE: 2923-613
; CURRENT APPLICATION NUMBER: US/10/490,955
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10881
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: EP 02 016 772.2
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: EP 02 006 712.0
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01 123 453.1
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 562
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 448
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: D. melanogaster or H. sapiens or M. musculus or C. elegans or
; OTHER INFORMATION: HeLa cells
US-10-490-955-448

Query Match   100.0%; Score 22; DB 10; Length 22;
Best Local Similarity   100.0%; Pred. No. 1.9;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
       ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 5
US-10-740-256A-62
; Sequence 62, Application US/10740256A
; Publication No. US20050074788A1
; GENERAL INFORMATION:
; APPLICANT: Dahlberg, James E.
; APPLICANT: Allawi, Hatim T.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson-Munoz, Marilyn
; APPLICANT: Chehak, LuAnne
; APPLICANT: Olson, Sarah M.
; TITLE OF INVENTION: Detection of Small Nucleic Acids
; FILE REFERENCE: FORS-08497
; CURRENT APPLICATION NUMBER: US/10/740,256A
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 62
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(22)
; OTHER INFORMATION: 2'-O-methyl
US-10-740-256A-62

Query Match   100.0%; Score 22; DB 10; Length 22;
Best Local Similarity   100.0%; Pred. No. 1.9;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
       ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
        |||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 6
US-10-909-125-269
; Sequence 269, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 22
; TYPE: RNA
; ORGANISM: H. sapiens
US-10-909-125-269

Query Match   100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
        |||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 7
US-10-909-125-369/c
; Sequence 369, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation

; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligomeric compound
US-10-909-125-369

Query Match   100.0%; Score 22; DB 10; Length 22;
Best Local Similarity   68.2%; Pred. No. 1.9;
Matches   15; Conservative   7; Mismatches   0; Indels   0; Gaps   0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
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Db   22 TAGCACGACAATAATGGTTTGTG 1

RESULT 8
US-10-881-362B-7
; Sequence 7, Application US/10881362B
; Publication No. US20060003337A1
; GENERAL INFORMATION:
; APPLICANT: Applied Biosystems
; TITLE OF INVENTION: Detection of Small RNAs
; FILE REFERENCE: 9692-000046
; CURRENT APPLICATION NUMBER: US/10/881,362B
; CURRENT FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 7
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-881-362B-7

Query Match   100.0%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
        |||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 9
US-11-055-035-16
; Sequence 16, Application US/11055035
; Publication No. US20050256072A1
; GENERAL INFORMATION:
; APPLICANT: ARONIN, NEIL
; APPLICANT: ZAMORE, PHILLIP D.
; APPLICANT: BRODERICK, JENNIFER
; TITLE OF INVENTION: DUAL FUNCTIONAL OLIGONUCLEOTIDES FOR USE IN REPRESSING
; TITLE OF INVENTION: MUTANT GENE EXPRESSION
; FILE REFERENCE: UMY-095
; CURRENT APPLICATION NUMBER: US/11/055,035
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: 60/543,467
; PRIOR FILING DATE: 2004-02-09

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;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn Ver. 3.3
;  SEQ ID NO 16
;  TYPE: RNA
;  LENGTH: 22
;  ORGANISM: Homo sapiens
US-11-055-035-16

Qy  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
    Best Local Similarity   100.0%;  Pred. No. 1.9;
    Matches   22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db  1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 10
US-11-102-453-15
; Sequence 15, Application US/11102453
; Publication No. US20050260648A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammatteo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: KLAUS2.006CP1
; CURRENT APPLICATION NUMBER: US/11/102,453
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/818,956
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-102-453-15

Qy  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
    Best Local Similarity   100.0%;  Pred. No. 1.9;
    Matches   22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db  1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 11
US-11-102-453-111
; Sequence 111, Application US/11102453
; Publication No. US20050260648A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammatteo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: KLAUS2.006CP1
; CURRENT APPLICATION NUMBER: US/11/102,453
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/818,956
; PRIOR FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Mus musculus
US-11-102-453-111


Qy  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
    Best Local Similarity   100.0%;  Pred. No. 1.9;
    Matches   22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db  1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 12
US-11-100-897-5
; Sequence 5, Application US/11100897
; Publication No. US20050272075A1
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, Nana
; APPLICANT: Kongsbak , Lars
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Echwald, Soren Morgenthaler
; APPLICANT: Mouritzen, Peter
; APPLICANT: Nielsen, Peter Stein
; APPLICANT: Norholm, Mikkel
; TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL
; TITLE OF INVENTION: INTERFERING RNAS
; FILE REFERENCE: 50287/013004
; CURRENT APPLICATION NUMBER: US/11/100,897
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/648,221
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 60/619,291
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/600,961
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/590,856
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/560,148
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-100-897-5

Qy  Query Match             100.0%;  Score 22;  DB 15;  Length 22;
    Best Local Similarity   100.0%;  Pred. No. 1.9;
    Matches   22;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db  1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 13
US-11-100-897-7
; Sequence 7, Application US/11100897
; Publication No. US20050272075A1
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, Nana
; APPLICANT: Kongsbak , Lars
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Echwald, Soren Morgenthaler
; APPLICANT: Mouritzen, Peter
; APPLICANT: Nielsen, Peter Stein
; APPLICANT: Norholm, Mikkel
; TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL
; TITLE OF INVENTION: INTERFERING RNAS
; FILE REFERENCE: 50287/013004
; CURRENT APPLICATION NUMBER: US/11/100,897
; CURRENT FILING DATE: 2005-04-07

Qy  Query Match             68.2%;  Score 22;  DB 15;  Length 22;
    Best Local Similarity   100.0%;  Pred. No. 1.9;
    Matches   15;  Conservative   7;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      :||||||||:||:|:|:::||:|
Db  1 TAGCAGCACATAATGTTTGTG 22
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; PRIOR APPLICATION NUMBER: 60/648,221
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 60/619,291
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: 60/600,961
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: 60/590,856
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/560,148
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
;
; SEQ ID NO 7
; LENGTH: 22
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence
US-11-100-897-7

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Qy   Query Match      100.0%;  Score 22;  DB 15;  Length 22;
     Best Local Similarity  100.0%;  Pred. No. 1.9;
     Matches  22;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db  1 UAGCAGCACAUAAUGGUUUGUG 22
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RESULT 14
US-11-100-897-73
Sequence 73, Application US/11100897
Publication No. US20050272075A1
GENERAL INFORMATION:
APPLICANT: Jacobsen, Nana
APPLICANT: Kongsbak , Lars
APPLICANT: Kauppinen, Sakari
APPLICANT: Echwald, Soren Morgenthaler
APPLICANT: Mouritzen, Peter
APPLICANT: Nielsen, Peter Stein
APPLICANT: Norholm, Mikkel
TITLE OF INVENTION: NOVEL METHODS FOR QUANTIFICATION OF microRNAS AND SMALL
TITLE OF INVENTION: INTERFERING RNAS
FILE REFERENCE: 50287/013004
CURRENT APPLICATION NUMBER: US/11/100,897
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/648,221
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 60/619,291
PRIOR FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: 60/600,961
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: 60/590,856
PRIOR FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: 60/560,148
PRIOR FILING DATE: 2004-04-07
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.3
SEQ ID NO 73
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-100-897-73

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Qy   Query Match      100.0%;  Score 22;  DB 15;  Length 22;
     Best Local Similarity  100.0%;  Pred. No. 1.9;
     Matches  22;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
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Db  1 UAGCAGCACAUAAUGGUUUGUG 22
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RESULT 15
US-11-171-175-131/c
Sequence 131, Application US/11171175
Publication No. US20060019286A1
GENERAL INFORMATION:
APPLICANT: Horvitz, H, Robert
APPLICANT: Miska, Eric A.
APPLICANT: Alvarez-Saavedra, Ezequiel A.
TITLE OF INVENTION: High Throughput Methods Relating to MicroRNA Expression Analysis
FILE REFERENCE: 01997/554003
CURRENT APPLICATION NUMBER: US/11/171,175
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/607,531
PRIOR FILING DATE: 2004-09-07
PRIOR APPLICATION NUMBER: 60/584,381
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-171-175-131

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Qy   Query Match      100.0%;  Score 22;  DB 16;  Length 22;
     Best Local Similarity  68.2%;  Pred. No. 1.9;
     Matches  15;  Conservative  7;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1 UAGCAGCACAUAAUGGUUUGUG 22
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Db 22 TAGCGAGCACATAATGGTTTGTG 1
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Search completed: November 2, 2006, 02:46:33
Job time : 528.371 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 1, 2006, 22:25:14 ; Search time 49.6571 Seconds
                 (without alignments)
                 859.641 Million cell updates/sec

Title: US-10-706-798-3
Perfect Score: 22
Sequence: 1 uagcagcacauaauguuugug 22
Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched: 2461376 seqs, 970166171 residues
Total number of hits satisfying chosen parameters: 4922752

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
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    2: /EMC_Celerra_SID53/ptodata/2/pubpna/US06_NEW_PUB.seq:*
    3: /EMC_Celerra_SID53/ptodata/2/pubpna/US07_NEW_PUB.seq:*
    4: /EMC_Celerra_SID53/ptodata/2/pubpna/US08_NEW_PUB.seq:*
    5: /EMC_Celerra_SID53/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
    6: /EMC_Celerra_SID53/ptodata/2/pubpna/US10_NEW_PUB.seq:*
    7: /EMC_Celerra_SID53/ptodata/2/pubpna/US11_NEW_PUB.seq:*
    8: /EMC_Celerra_SID53/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
    9: /EMC_Celerra_SID53/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
   10: /EMC_Celerra_SID53/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	22	100.0	22	6	US-10-818-956-15	Sequence 15, Appl
2	22	100.0	22	6	US-10-818-956-111	Sequence 111, Appl
3	22	100.0	22	7	US-11-194-055-35	Sequence 35, Appl
4	22	100.0	22	7	US-11-317-660-795	Sequence 795, App
5	22	100.0	22	7	US-11-084-082-2	Sequence 2, Appli
6	22	100.0	22	7	US-11-084-082-27	Sequence 27, Appl
7	22	100.0	22	8	US-11-242-139-31	Sequence 31, Appl
8	22	100.0	22	9	US-11-242-139-127	Sequence 127, Appl
9	22	100.0	22	8	US-11-375-650-3	Sequence 3, Appl
10	22	100.0	40	8	US-11-194-055-325	Sequence 325, App
11	22	100.0	78	7	US-11-084-082-26	Sequence 26, Appl
12	22	100.0	83	8	US-11-194-055-33	Sequence 33, Appl
13	22	100.0	83	9	US-11-375-650-1	Sequence 1, Appl
14	22	100.0	108	8	US-11-194-055-32	Sequence 32, Appl
15	22	100.0	347503	8	US-11-266-748A-23474	Sequence 23474, A
16	18.8	85.5	7808	6	US-10-959-175-4	Sequence 4, Appl
17	18.8	85.5	7824	6	US-10-959-175-5	Sequence 5, Appli
18	18	81.8	23	9	US-11-375-650-5	Sequence 5, Appli
19	17.8	80.9	1200	8	US-11-266-748A-302054	Sequence 302054,
20	17.4	79.1	22	7	US-10-818-956-112	Sequence 112, Appl
21	17.4	79.1	22	6	US-11-317-660-37	Sequence 37, Appl
22	17.4	79.1	22	7	US-11-317-660-796	Sequence 796, App
23	17.4	79.1	22	8	US-11-242-139-128	Sequence 128, App
24	17.4	79.1	40	8	US-11-194-055-327	Sequence 327, Appl
25	17.4	79.1	64	8	US-11-194-055-34	Sequence 34, Appl
26	17.2	78.2	98	8	US-11-194-055-35	Sequence 35, Appl
27	17.2	78.2	132	8	US-11-266-748A-119432	Sequence 119432,
28	16.4	74.5	1000	8	US-11-266-748A-221650	Sequence 221650,
29	16.4	74.5	1000	8	US-11-266-748A-286791	Sequence 286791,
30	16.4	74.5	1000	8	US-11-266-748A-338220	Sequence 338220,
31	16.4	74.5	1000	8	US-11-266-748A-397338	Sequence 397338,
32	16.4	74.5	34161	8	US-10-539-228-436	Sequence 436, App
33	16.4	74.5	34160	8	US-10-539-228-383	Sequence 383, App
34	16.4	74.5	43179	6	US-10-284-444-12515	Sequence 12515, A
35	16.2	73.6	201	6	US-10-284-444-12517	Sequence 12517, A
36	16.2	73.6	201	7	US-11-244-330A-2226	Sequence 2226, Ap
37	16.2	73.6	335	7	US-11-266-748A-100416	Sequence 100416,
38	16.2	73.6	493	8	US-11-266-748A-153227	Sequence 153227,
39	16.2	73.6	493	8	US-10-471-571A-29965	Sequence 29965, Ap
40	16.2	73.6	585	6	US-11-266-748A-299464	Sequence 299464,
41	16.2	73.6	664	8	US-11-266-748A-91874	Sequence 91874, A
42	16.2	73.6	879	8	US-11-266-748A-144685	Sequence 144685, A
43	16.2	73.6	879	8	US-11-266-748A-48314	Sequence 48314, A
44	16.2	73.6	916	8	US-11-266-748A-224816	Sequence 224816,
45	16.2	73.6	1000	8	US-11-266-748A-224816	Sequence 224816,

ALIGNMENTS

RESULT 1
US-10-818-956-15
; Sequence 15, Application US/10818956
; Publication No. US20060134639A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammatteo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: KLAUS2.006AUS
; CURRENT APPLICATION NUMBER: US/10/818,956
; CURRENT FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-818-956-15

Query Match   100.0%; Score 22; DB 6; Length 22;
Best Local Similarity   100.0%;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 UAGCAGCACAUAAUGUUUGUG 22
         ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGUUUGUG 22

RESULT 2
US-10-818-956-111
; Sequence 111, Application US/10818956
; Publication No. US20060134639A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammatteo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: KLAUS2.006AUS
; CURRENT APPLICATION NUMBER: US/10/818,956
; CURRENT FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 212

SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-818-956-111

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

Query Match   100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-818-956-111

RESULT 3
US-11-317-660-36
Sequence 36, Application US/11317660
Publication No. US20060185027A1
GENERAL INFORMATION:
; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-RHOADES, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURGE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING MIRNA TARGETS
; TITLE OF INVENTION: AND FOR ALTERING MIRNA AND TARGET EXPRESSION
; FILE REFERENCE: W0571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: 60/639,231
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-317-660-36

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

Query Match   100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-11-317-660-36

RESULT 4
US-11-317-660-795/c
Sequence 795, Application US/11317660
Publication No. US20060185027A1
GENERAL INFORMATION:
; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-RHOADES, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURGE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING MIRNA TARGETS
; TITLE OF INVENTION: AND FOR ALTERING MIRNA AND TARGET EXPRESSION
; FILE REFERENCE: W0571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: 60/639,231
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 795
; LENGTH: 22
; TYPE: RNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-317-660-795

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||:||:||:|:||:|
Db 22 TAGCAGCACATAATGGTTTGTG 1

Query Match   68.2%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 15; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

US-11-317-660-795

RESULT 5
US-11-084-082-2
Sequence 2, Application US/11084082
Publication No. US20060211000A1
GENERAL INFORMATION:
; APPLICANT: SORGE, JOSEPH A.
; APPLICANT: MULLINAX, REBECCA L.
; TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF
; TITLE OF INVENTION: MICRORNA
; FILE REFERENCE: STG-114
; CURRENT APPLICATION NUMBER: US/11/084,082
; CURRENT FILING DATE: 2005-03-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-084-082-2

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

Query Match   100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-11-084-082-2

RESULT 6
US-11-084-082-27
Sequence 27, Application US/11084082
Publication No. US20060211000A1
GENERAL INFORMATION:
; APPLICANT: SORGE, JOSEPH A.
; APPLICANT: MULLINAX, REBECCA L.
; TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF
; TITLE OF INVENTION: MICRORNA
; FILE REFERENCE: STG-114
; CURRENT APPLICATION NUMBER: US/11/084,082
; CURRENT FILING DATE: 2005-03-21
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 27
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-084-082-27

Qy 1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db 1 UAGCAGCACAUAAUGGUUUGUG 22

Query Match   100.0%; Score 22; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-11-242-139-31
Sequence 31, Application US/11242139
Publication No. US20060099619A1
GENERAL INFORMATION:
APPLICANT: REMACLE, JOSE
APPLICANT: DU LONGEVILLE, FRANCOISE
APPLICANT: HAMELS, SANDRINE
TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MIRNA ON MICRO-ARRAYS
FILE REFERENCE: 03642-0107
CURRENT APPLICATION NUMBER: US/11,242,139
CURRENT FILING DATE: 2005-10-04
PRIOR APPLICATION NUMBER: 10/637,656
PRIOR FILING DATE: 2003-08-11
NUMBER OF SEQ ID NOS: 239
SOFTWARE: Patentin version 3.3
SEQ ID NO 31
LENGTH: 22
TYPE: RNA
ORGANISM: Homo sapiens
US-11-242-139-31

Query Match   100.0%;   Score 22;   DB 8;   Length 22;
Best Local Similarity   100.0%;   Pred. No. 0.093;
Matches   22;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 8
US-11-242-139-127
Sequence 127, Application US/11242139
Publication No. US20060099619A1
GENERAL INFORMATION:
APPLICANT: REMACLE, JOSE
APPLICANT: DU LONGEVILLE, FRANCOISE
APPLICANT: HAMELS, SANDRINE
TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MIRNA ON MICRO-ARRAYS
FILE REFERENCE: 03642-0107
CURRENT APPLICATION NUMBER: US/11,242,139
CURRENT FILING DATE: 2005-10-04
PRIOR APPLICATION NUMBER: 10/637,656
PRIOR FILING DATE: 2003-08-11
NUMBER OF SEQ ID NOS: 239
SOFTWARE: Patentin version 3.3
SEQ ID NO 127
LENGTH: 22
TYPE: RNA
ORGANISM: Mus musculus
US-11-242-139-127

Query Match   100.0%;   Score 22;   DB 8;   Length 22;
Best Local Similarity   100.0%;   Pred. No. 0.093;
Matches   22;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 9
US-11-375-650-3
Sequence 3, Application US/11375650
Publication No. US20060165659A1
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
APPLICANT: Calin, George A.
TITLE OF INVENTION: Compositions and Methods for Cancer
TITLE OF INVENTION: Diagnosis and Therapy
FILE REFERENCE: 08321-0126US1
CURRENT APPLICATION NUMBER: US/11,375,650
CURRENT FILING DATE: 2006-03-13
PRIOR APPLICATION NUMBER: US/10/706,798
PRIOR FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/425,864
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/469,464
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 22
TYPE: RNA
ORGANISM: Homo sapiens
US-11-375-650-3

Query Match   100.0%;   Score 22;   DB 9;   Length 22;
Best Local Similarity   100.0%;   Pred. No. 0.093;
Matches   22;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

RESULT 10
US-11-194-055-325
Sequence 325, Application US/11194055
Publication No. US20060105360A1
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
APPLICANT: Liu, Chang-Gong
APPLICANT: Calin, George, A.
APPLICANT: Cinzia, Sevignani
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
FEATURES
FILE REFERENCE: 3589.1018-008
CURRENT APPLICATION NUMBER: US/11/194,055
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: PCT/US2005/004865
PRIOR FILING DATE: 2005-02-09
PRIOR APPLICATION NUMBER: 60/543,119
PRIOR FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/542,929
PRIOR FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/542,963
PRIOR FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/542,940
PRIOR FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/580,959
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/580,797
PRIOR FILING DATE: 2004-06-18
NUMBER OF SEQ ID NOS: 663
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 325
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide probe
US-11-194-055-325

Query Match   68.2%;   Score 22;   DB 8;   Length 40;
Best Local Similarity   100.0%;   Pred. No. 0.1;
Matches   15;   Conservative   7;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 UAGCAGCACAUAAUGGUUUGUG 22
      ||||||||||||||||||||||
Db   1 UAGCAGCACAUAAUGGUUUGUG 22

```
Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :||||||||||:|:|::|:||:|
Db         14 TAGCAGCACATAATGGTTTGTG 35
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RESULT 11
US-11-084-082-26/c
; Sequence 26, Application US/11084082
; Publication No. US20060211000A1
; GENERAL INFORMATION:
;   APPLICANT: SORGE, JOSEPH A.
;   APPLICANT: MULLINAX, REBECCA L.
;   TITLE OF INVENTION: METHODS, COMPOSITIONS, AND KITS FOR DETECTION OF
;   TITLE OF INVENTION: MICRORNA
;   FILE REFERENCE: STG-114
;   CURRENT APPLICATION NUMBER: US/11/084,082
;   CURRENT FILING DATE: 2005-03-21
;   NUMBER OF SEQ ID NOS: 41
;   SOFTWARE: Patentin Ver. 3.3
; US-11-084-082-26
;
;   SEQ ID NO 26
;   LENGTH: 78
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: oligonucleotide

US-11-084-082-26

Query Match   100.0%; Score 22; DB 7; Length 78;
Best Local Similarity   68.2%; Pred. No. 0.11;
Matches   15; Conservative   7; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :||||||||||:|:|::|:||:|
Db         49 TAGCAGCACATAATGGTTTGTG 28
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Query Match   100.0%; Score 22; DB 8; Length 83;
Best Local Similarity   68.2%; Pred. No. 0.11;
Matches   15; Conservative   7; Mismatches   0; Indels   0; Gaps   0;

RESULT 13
US-11-375-650-1
; Sequence 1, Application US/11375650
; Publication No. US20060165659A1
; GENERAL INFORMATION:
;   APPLICANT: Croce, Carlo M.
;   APPLICANT: Calin, George A.
;   TITLE OF INVENTION: Compositions and Methods for Cancer
;   TITLE OF INVENTION: Diagnosis and Therapy
;   FILE REFERENCE: 08321-0126US1
;   CURRENT APPLICATION NUMBER: US/11/375,650
;   CURRENT FILING DATE: 2006-03-13
;   PRIOR APPLICATION NUMBER: US/10/706,798
;   PRIOR FILING DATE: 2003-11-12
;   PRIOR APPLICATION NUMBER: 60/425,864
;   PRIOR FILING DATE: 2002-11-13
;   PRIOR APPLICATION NUMBER: 60/469,464
;   PRIOR FILING DATE: 2003-05-09
;   NUMBER OF SEQ ID NOS: 54
;   SOFTWARE: FastSEQ for Windows Version 4.0
; US-11-375-650-1
;
;   SEQ ID NO 1
;   LENGTH: 83
;   TYPE: RNA
;   ORGANISM: Homo sapiens

RESULT 12
US-11-194-055-33
; Sequence 33, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
;   APPLICANT: Croce, Carlo M.
;   APPLICANT: Liu, Chang-Gong
;   APPLICANT: Calin, George, A.
;   APPLICANT: Cinzia, Sevignani
;   TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
;   TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
;   TITLE OF INVENTION: FEATURES
;   FILE REFERENCE: 3589.1018-008
;   CURRENT APPLICATION NUMBER: US/11/194,055
;   CURRENT FILING DATE: 2005-07-29
;   PRIOR APPLICATION NUMBER: PCT/US2005/004865
;   PRIOR FILING DATE: 2005-02-09
;   PRIOR APPLICATION NUMBER: 60/543,119
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,929
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,963
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,940
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,959
;   PRIOR FILING DATE: 2004-06-18
;   PRIOR APPLICATION NUMBER: 60/580,797
;   PRIOR FILING DATE: 2004-06-18
;   NUMBER OF SEQ ID NOS: 663
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 33
;   LENGTH: 83
;   TYPE: DNA
;   ORGANISM: Homo sapiens
; US-11-194-055-33

```
Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :||||||||||:|:|::|:||:|
Db         14 TAGCAGCACATAATGGTTTGTG 35
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Query Match   100.0%; Score 22; DB 9; Length 83;
Best Local Similarity   100.0%; Pred. No. 0.11;
Matches   22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 14
US-11-194-055-32
; Sequence 32, Application US/11194055
; Publication No. US20060105360A1
; GENERAL INFORMATION:
;   APPLICANT: Croce, Carlo M.
;   APPLICANT: Liu, Chang-Gong
;   APPLICANT: Calin, George, A.
;   APPLICANT: Cinzia, Sevignani
;   TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCERS WITH
;   TITLE OF INVENTION: MicroRNA LOCATED IN OR NEAR CANCER-ASSOCIATED CHROMOSOMAL
;   TITLE OF INVENTION: FEATURES
;   FILE REFERENCE: 3589.1018-008
;   CURRENT APPLICATION NUMBER: US/11/194,055
;   CURRENT FILING DATE: 2005-07-29
;   PRIOR APPLICATION NUMBER: PCT/US2005/004865
;   PRIOR FILING DATE: 2005-02-09
;   PRIOR APPLICATION NUMBER: 60/543,119
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,929
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,963
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,940
;   PRIOR FILING DATE: 2004-02-09
;   PRIOR APPLICATION NUMBER: 60/542,959
;   PRIOR FILING DATE: 2004-06-18
;   PRIOR APPLICATION NUMBER: 60/580,797
```

```
Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              ||||||||||||||||||||||
Db         14 UAGCAGCACAUAAUGGUUUGUG 35
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;    PRIOR FILING DATE: 2004-06-18
;    NUMBER OF SEQ ID NOS: 663
;    SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 32
;    LENGTH: 108
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-194-055-32

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :|||||||||:|:||:::||:|
Db         43 TAGCAGCACATAAATGGTTTGTG 64

Query Match             100.0%;  Score 22;  DB 8;  Length 108;
Best Local Similarity    68.2%;  Pred. No. 0.12;
Matches   15;  Conservative   7;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 15
US-11-266-748A-23474/c
; Sequence 23474, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;    APPLICANT: Harkin, Paul
;    APPLICANT: Johnston, Patrick
;    APPLICANT: Mulligan, Karl
;    TITLE OF INVENTION: Transcriptome Microarray Technology and
;    TITLE OF INVENTION: Methods of Using the Same
;    FILE REFERENCE: 55815-0102 (319189)
;    CURRENT APPLICATION NUMBER: US/11/266,748A
;    CURRENT FILING DATE: 2005-11-03
;    PRIOR APPLICATION NUMBER: EP 04105479.2
;    PRIOR FILING DATE: 2004-11-03
;    PRIOR APPLICATION NUMBER: EP 04105482.6
;    PRIOR FILING DATE: 2004-11-03
;    PRIOR APPLICATION NUMBER: EP 04105483.4
;    PRIOR FILING DATE: 2004-11-03
;    PRIOR APPLICATION NUMBER: EP 04105507.0
;    PRIOR FILING DATE: 2004-11-03
;    PRIOR APPLICATION NUMBER: EP 04105485.9
;    PRIOR FILING DATE: 2004-11-03
;    PRIOR APPLICATION NUMBER: EP 04105484.2
;    PRIOR FILING DATE: 2004-11-03
;    PRIOR APPLICATION NUMBER: US 60/662,276
;    PRIOR FILING DATE: 2005-03-14
;    PRIOR APPLICATION NUMBER: US 60/700,293
;    PRIOR FILING DATE: 2005-07-18
;    NUMBER OF SEQ ID NOS: 483996
;    SOFTWARE: PatentIn version 3.3
;
; SEQ ID NO 23474
;    LENGTH: 347503
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-11-266-748A-23474

Qy          1 UAGCAGCACAUAAUGGUUUGUG 22
              :||||||||||:||:||::||:|
Db      52185 TAGCAGCACATAAATGGTTTGTG 52164

Query Match             100.0%;  Score 22;  DB 8;  Length 347503;
Best Local Similarity    68.2%;  Pred. No. 0.41;
Matches   15;  Conservative   7;  Mismatches   0;  Indels   0;  Gaps   0;

Search completed: November 1, 2006, 22:36:58
Job time : 50.6571 secs
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